

WO 03/072014

PCT/US02/16877

1441

CGTGATGCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGC
GCTAC

481 R D A C T Y A T A L N V A S L S V E R Y

5

1501

TTGGCCATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCA
AGAAA

501 L A I C H P F K A K T L M S R S R T K K

10

1561

TTTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTCAC
CATG

521 F I S A I W L A S A L L A I P M L F T M

15

1621

GGCCTGCAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACAC
CCATT

541 G L Q N R S G D G T H P G G L V C T P I

20

1681

GTGGACACAGCCACTGTCAAGGTCGTCATCCAGGTTAACACCTTCATGTCCTTCCT
GTTT

561 V D T A T V K V V I Q V N T F M S F L F

25

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1741

CCCATGTTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCAT
GGTG

581 P M L V I S I L N T V I A N K L T V M V

5

1801

CACCAGGCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACACAACGGTTTAG
AGCAC

601 H Q A A E Q G R V C T V G T H N G L E H

10

1861

AGCACGTTCAACATGACCATCGAGCCGGGTGCTGCCAGGCCCTGCGCCACGGAG
TCCTC

621 S T F N M T I E P G R V Q A L R H G V L

15

1921

GTCTTACGTGCTGTGGTCATTGCCTTTGTGGTCTGCTGGCTGCCCTACCACGTGCG
ACGC

641 V L R A V V I A F V V C W L P Y H V R R

20

1981

CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTCTA
CCAC

661 L M F C Y I S D E Q W T T F L F D F Y H

25

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2041

TATTTCTACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCAT
CCTC

681 Y F Y M L T N A L F Y V S S A I N P I L

5

2101

TACAACCTGGTCTCCGCCAACTTCCGCCAGGTCCTTCTGTCCACGCTGGCCTGCCT
TTGT

701 Y N L V S A N F R Q V F L S T L A C L C

10

2161

CCTGGGTGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCAGGAAGCCCAACA
GCATG

721 P G W R H R R K K R P T F S R K P N S M

15

NotI +2 TrxA

2221

TCCAGCAACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgeggccgcaA
GC

20

741 S S N H A F S T S A T R E T L Y A A A S

2281

GATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGG
ACGGG

25

761 D K I I H L T D D S F D T D V L K A D G

PCT/US02/16877

GCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCC
 CGATT

5 781 A I L V D F W A E W C G P C K M I A P I

CTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACA
TCGAT

10 801 L D E I A D E Y Q G K L T V A K L N I D

CAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCC GACTCTGCTGC
TGTTCT

15 821 Q N P G T A P K Y G I R G I P T L L L F

AAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGA
AAGAG

20 841 K N G E V A A T K V G A L S K G O L K E

NotI +2 Flag stop

25 TTCCTCGACGCTAACCTGGCGcgggccgcaGATTATAAAGATGACGATGACAAATAAT
AA

WO 03/072014

PCT/US02/16877

861 F L D A N L A A A A D Y K D D D D K * *

KpnI

2641 GGTACC

5

SEQ ID NO.: 170

10 MalE (1-28) Factor Xa NTR (43-424) TrxA (2-109) FLAG

Sall +1 MalE leader (1-28)

1

gtcgacATGAAAATAAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACG

15 ATGATGTTT

1 M K I K T G A R I L A L S A L T T M M F

Factor Xa +43 NTR

61

20 TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCACCTCGGAATCCGACACGG
CAGGG

21 S A S A L A K I I E A R T S E S D T A G

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121

CCCAACAGCGACCTGGACGTGAACACTGACATTTATTCCAAGGTGCTGGTGACTG
CTATA

41 P N S D L D V N T D I Y S K V L V T A I

5

181

TACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACTCT
AGCG

61 Y L A L F V V G T V G N S V T A F T L A

10

241

CGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACCTGGGCAGCC
TGGCA

81 R K K S L Q S L Q S T V H Y H L G S L A

15

301

CTGTGCGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTCAT
CTGG

101 L S D L L I L L L A M P V E L Y N F I W

20

361

GTACACCATCCCTGGGCCTTGGGGACGCTGGCTGCCGTGGCTACTATTTCCTGCG
TGAT

121 V H H P W A F G D A G C R G Y Y F L R D

25

WO 03/072014

PCT/US02/16877

421

GCCTGCCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACT
TGGCC

141 A C T Y A T A L N V A S L S V E R Y L A

5

481

ATCTGCCATCCCTTCAAGGCCAAGACCCTCATGTCCCGCAGCCGCACCAAGAAAT
TCATC

161 I C H P F K A K T L M S R S R T K K F I

10

541

AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTACCATGGG
CCTG

181 S A I W L A S A L L A I P M L F T M G L

15

601

CAGAACCGCAGTGGTGACGGCACGCACCCTGGCGGCCTGGTGTGCACACCCATTG
TGGAC

201 Q N R S G D G T H P G G L V C T P I V D

20

661

ACAGCCACTGTCAAGGTCGTATCCAGGTTAACACCTTCATGTCTTCCTGTTTCC
CATG

221 T A T V K V V I Q V N T F M S F L F P M

25

PCT/US02/16877

TTGGTCATCTCCATCCTAAACACCGTGATTGCCAACAACTGACAGTCATGGTGCA
CCAG

241 L V I S I L N T V I A N K L T V M V H Q

5

GCCGCCGAGCAGGGCCGAGTGTGCACCGTGGGCACACAACGGTTTAGAGCACA
GCACG

261 A A E Q G R V C T V G T H N G L E H S T

10

TTCAACATGACCATCGAGCCGGGTCGTGTCCAGGCCCTGCGCCACGGAGTCCTCG
TCTTA

281 F N M T I E P G R V Q A L R H G V L V L

15

CGTGCTGTGGTCATTGCCCTTGTGGTCTGCTGGCTGCCCTACCACGTGCGACGCCT
GATG

301 R A V V I A F V V C W L P Y H V R R L M

20

TTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTCGATTCTACCACTA
TTTC

321 F C Y I S D E Q W T T F L F D F Y H Y F

25

WO 03/072014

PCT/US02/16877

1021

TACATGCTAACCAACGCTCTCTTCTACGTCAGCTCCGCCATCAATCCCATCCTCTA
CAAC

341 Y M L T N A L F Y V S S A I N P I L Y N

5

1081

CTGGTCTCCGCCAACTTCCGCCAGGTCTTTCTGTCCACGCTGGCCTGCCTTTGTCC
TGGG

361 L V S A N F R Q V F L S T L A C L C P G

10

1141

TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACAGCATGT
CCAGC

381 W R H R R K K R P T F S R K P N S M S S

15

NotI +2 TrxA

1201

AACCATGCCTTTTCCACCAGCGCCACCCGGGAGACCCTGTACgcggcgcaAGCGATA
AA

20

401 N H A F S T S A T R E T L Y A A A S D K

1261

ATTATTACCTGACTGACGACAGTTTGTACACGGATGTACTCAAAGCGGACGGGG
CGATC

25

421 I I H L T D D S F D T D V L K A D G A I

WO 03/072014

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1321

CTCGTCGATTCTGGGCAGAGTGGTGC GGTCCTGCAAAATGATCGCCCCGATTCT
GGAT

5 441 L V D F W A E W C G P C K M I A P I L D

1381

GAAATCGCTGACGAATATCAGGGCAAAC TGACCGTTGCAAAACTGAACATCGATC
AAAC

10 461 E I A D E Y Q G K L T V A K L N I D Q N

1441

CCTGGCACTGCGCCGAAATATGGCATCCG TGGTATCCCGACTCTGCTGCTGTTCAA
AAAC

15 481 P G T A P K Y G I R G I P T L L L F K N

1501

GGTGAAAGTGGCGGCAACCAAAGTGGGTG CACTGTCTAAAGGTCAGTTGAAAGAGT
TCCTC

20 501 G E V A A T K V G A L S K G Q L K E F L

NotI Flag stop KpnI

1561

GACGCTAACCTGGCAgcggccgcaGATTATAAAGATGACGATGACAAATAATAAGGTA
25 CC

WO 03/072014

PCT/US02/16877

521 D A N L A A A A D Y K D D D D K

5 SEQ ID NO.: 188

Human 2AR GS1 chimeric fusion

SalI +1 B2AR

10 1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
 TGGCACCCAA TGGAAGCCAT

 61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
 GGGTGGTGGG CATGGGCATC

15 121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
 TGCTGGTCAT CACAGCCATT

 181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
 TCACTTCACT GGCCTGTGCT

 241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
20 CCCATATTCT TATGAAAATG

 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
 TTGATGTGCT GTGCGTCACG

 361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT
 ACTTTGCCAT TACTTCACCT

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PCT/US02/16877

- 421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG
TGATCATTCT GATGGTGTGG
- 481 ATTGTGTCAG GCCTTAYCTC CTTCTGCCC ATTCAGATGC
ACTGGTACAG GGCCACCCAC
- 5 541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG
ACTTCTTCAC GAACCAAGCC
- 601 TATGCCATTG CCTCTTCCAT CGTGTCCITC TACGTTCCCC
TGGTGATCAT GGTCTTCGTC
- 661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA
10 AGATTGACAA ATCTGAGGGC
- 721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG
GGCGGACGGG GCATGGACTC
- 781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC
TCAAGACGTT AGGCATCATC
- 15 841 ATGGGCAC TTACCCCTCTG CTGGCTGCCC TTCTTCATCG
TTAACAATTGT GCATGTGATC
- 901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCTTAA
ATTGGATAGG CTATGTCAAT
- 961 TCTGGTTTCA ATCCCTTAT CTA CTGCGCGG AGCCCAGATT
20 TCAGGATTGC CTTCCAGGAG
- 1021 CTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA
ATGGCTACTC CAGCAACGGC
- 1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA
AAGAAAATAA ACTGCTGTGT
- 25 1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG
GTACTGTGCC TAGCGATAAC

WO 03/072014

PCT/US02/16877

Last B2AR Linker

sequence

1201 ATTGATTAC AAGGGAGGAA TTGTAGTACA AATGACTCAC
5 TGCTAGAGCG TGGCCAGACG

PstI XhoI +2 GS1 alpha

1261 GTCACCAACC TGCAGCTCGA GGGCTGCCTC GGGAACAGTA
AGACCGAGGA CCAGCGCAAC

10

1321 GAGGAGAAGG CGCAGCGTGA GGCCAACAAA AAGATCGAGA
AGCAGCTGCA GAAGGACAAG

1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG
15 CTGGAGAATC TGGTAAAAGC

1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT
TTAATGGAGA CAGTGAGAAG

1501 GCAACCAAAG TGCAGGACAT CAAAACAAC CTGAAAGAGG
CGATTGAAAC CATGTGGCC

1561 GCCATGAGCA ACCTGGTGCC CCCCCTGGAG CTGGCCAACC
20 CCGAGAACCA GTTCAGAGTG

1621 GACTACATCC TGAGTGTGAT GAACGTGCCT GACTTTGACT
TCCCTCCCGA ATTCTATGAG

1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCGTGCCT
25 GCTACGAACG CTCCAACGAG

WO 03/072014

PCT/US02/16877

1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA
TCGACGTGAT CAAGCAGGCT

1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTGCCGTG
TCCTGACTTC TGGAAATCTTT

5 1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT
TTGACGTGGG TGGCCAGCGC

1921 GATGAACGCC GCAAGTGGAT CCAGTGCTTC AACGATGTGA
TGCCCATCAT CTTCGTGGTG

1981 GCCAGCAGCA GCTACAACAT GGTCATCCGG GAGGACAACC
10 AGACCAACCG CCTGCAGGAG

2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC
TGCGCACCAT CTCTGTGATC

2101 CTGTTCTCA ACAAGCAAGA TCTGCTCGCT GAGAAAGTCC
TTGCTGGGAA ATCGAAGATT

15 2161 GAGGACTACT TTCCAGAATT TGCTCGCTAC ACTACTCCTG
AGGATGCTAC TCCCGAGCCC

2221 GGAGAGGACC CACGCGTGAC CCGGGCCAAG TACTTCATTC
GAGATGAGTT TCTGAGGATC

2281 AGCACTGCCA GTGGAGATGG GCGTCACTAC TGCTACCCTC
20 ATTTACCTCG CGCTGTGGAC

2341 ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA
TCATTACGCG CATGCACCTT

25 2401 CGTCAGTACG AGCTGCTCAT CGATTAATAA TCTAGAGGAT
CCCCGCGCCC TCATCCGAAA

ClaI Stop XbaI

Stem-loop

WO 03/072014

PCT/US02/16877

2461 GGGCG

5

SEQ ID NO.: 190

Human 2AR stop GS1 transcriptional fusion

10

PstI +1 B2AR

1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
TGGCACCCAA TGGAAGCCAT

15

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
TGCTGGTCAT CACAGCCATT

20

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
CCCATATTCT TATGAAAATG

301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
TTGATGTGCT GTGCGTCACG

PCT/US02/16877

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG

481 ATTGTGTCAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG

601 TATGCCATTG CCTCTTCCAT CGTGTCCTTC TACGTTCCCC

661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA

721 CGTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC

841 ATGGGCACTT TCACCCTCTG CTGGCTGCCC TTCTTCATCG

901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA

961 TCTGGTTTCA ATCCCCTTAT CTACTGCCGG AGCCCAGATT

1021 CTTCTGTGCC TGC GCAGGTC TTCTTTGAAG GCCTATGGCA

1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA

PCT/US02/16877

sequence Last B2AR Linker

PstI Stop SD XhoI +2 GS1 alpha

1321 AGACCGAGGA CCAGCGCAAC GAGGAGAAGG CGCAGCGTGA
15 GGCCAACAAA AAGATCGAGA

1441 CTGGAGAATC TGGTAAAAGC ACCATTGTGA AGCAGATGAG
GATCCTGCAT GTTAATGGGT

1561 CGATTGAAAC CATTGTGGCC GCCATGAGCA ACCTGGTGCC
CCCCGTGGAG CTGGCCAACC

114/268

WO 03/072014

PCT/US02/16877

1681 TCCCTCCCGA ATTCTATGAG CATGCCAAGG CTCTGTGGGA
GGATGAAGGA GTGCGTGCCT

1741 GCTACGAACG CTCCAACGAG TACCAGCTGA TTGACTGTGC
CCAGTACTTC CTGGACAAGA

5 1801 TCGACGTGAT CAAGCAGGCT GACTATGTGC CGAGCGATCA
GGACCTGCTT CGCTGCCGTG

1861 TCCTGACTTC TGGAATCTTT GAGACCAAGT TCCAGGTGGA
CAAAGTCAAC TTCCACATGT

1921 TTGACGTGGG TGGCCAGCGC GATGAACGCC GCAAGTGGAT
10 CCAGTGCTTC AACGATGTGA

1981 CTGCCATCAT CTTCTGGTGT GCCAGCAGCA GCTACAACAT
GGTCATCCGG GAGGACAACC

2041 AGACCAACCG CCTGCAGGAG GCTCTGAACC TCTTCAAGAG
CATCTGGAAC AACAGATGGC

15 2101 TGCGCACCAT CTCTGTGATC CTGTTCTCA ACAAGCAAGA
TCTGCTCGCT GAGAAAGTCC

2161 TTGCTGGGAA ATCGAAGATT GAGGACTACT TTCCAGAATT
TGCTCGCTAC ACTACTCCTG

2221 AGGATGCTAC TCCCAGAGCCC GGAGAGGACC CACGCGTGAC
20 CCGGGCCAAG TACTTCATTC

2281 GAGATGAGTT TCTGAGGATC AGCACTGCCA GTGGAGATGG
GCGTCACTAC TGCTACCCTC

2341 ATTTACCTG CGCTGTGGAC ACTGAGAACA TCCGCCGTGT
GTTCACGAC TGCCGTGACA

25

ClaI Stop XbaI

PCT/US02/16877

Stem-loop

5 2461 CCCC GCGCCC TCATCCGAAA GGGCG

SEQ ID NO.: 192

10

Human GS1

XhoI

1

15 C TCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG
AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

61

20 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG
GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

WO 03/072014

PCT/US02/16877

121

CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

41 H R L L L L G A G E S G K S T I V K Q M

5

181

AGGATCCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACCAAAGTGC
AGGAC

61 R I L H V N G F N G D S E K A T K V Q D

10

241

ATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACC
TGGTG

81 I K N N L K E A I E T I V A A M S N L V

15

301

CCCCCGTGGAGCTGGCCAACCCGAGAACCAGTTCAGAGTGGACTACATCCTGA
GTGTG

101 P P V E L A N P E N Q F R V D Y I L S V

20

361

ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCT
GTGG

121 M N V P D F D F P P E F Y E H A K A L W

25

WO 03/072014

PCT/US02/16877

421

GAGGATGAAGGAGTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTG
ACTGT

141 E D E G V R A C Y E R S N E Y Q L I D C

5

481

CCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTCCGA
GCGAT

161 A Q Y F L D K I D V I K Q A D Y V P S D

10

541

CAGGACCTGCTTCGCTGCCGTGCTGACTTCTGGAATCTTTGAGACCAAGTTCCA
GGTG

181 Q D L L R C R V L T S G I F E T K F Q V

15

601

GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCATGAACGCCGCA
ATGTG

201 D K V N F H M F D V G G Q R D E R R K W

20

661

ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTA
CAAC

221 I Q C F N D V T A I I F V V A S S S Y N

25

WO 03/072014

PCT/US02/16877

721

ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCT
TCAAG

241 M V I R E D N Q T N R L Q E A L N L F K

5

781

AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCTCAACA
AGCAA

261 S I W N N R W L R T I S V I L F L N K Q

10

841

GATCTGCTCGCTGAGAAAGTCCTTGCTGGGAAATCGAAGATTGAGGACTACTTTC
CAGAA

281 D L L A E K V L A G K S K I E D Y F P E

15

901

TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCAGCCCGAGAGGACCCAC
CGGTG

301 F A R Y T T P E D A T P E P G E D P R V

20

961

ACCCGGGCCAAGTACTTCATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTG
GAGAT

321 T R A K Y F I R D E F L R I S T A S G D

25

WO 03/072014

PCT/US02/16877

1021

GGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCG
CCGT

341 G R H Y C Y P H F T C A V D T E N I R R

5

1081

GTGTTCAACGACTGCCGTGACATCATTACGCGCATGCACCTTCGTCAGTACGAGCT
GCTC

361 V F N D C R D I I Q R M H L R Q Y E L L

10

ClaI

ATCGAT

15

SEQ ID NO.: 193

Human GS2

XhoI

20

1

CTCGAGATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCGCAACGAGGAG
AAGGCGCAGCGT

1 M G C L G N S K T E D Q R N E E K A Q R

WO 03/072014

PCT/US02/16877

61

GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGG
GCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

5

121

CACCGCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGC
AGATG

41 H R L L L L G A G E S G K S T I V K Q M

10

181

AGGATCCTGCATGTTAATGGGTTTAATGGAGAGGGCGGCGAAGAGGACCCGACGG
CTGCA

61 R I L H V N G F N G E G G E E D P Q A A

15

241

AGGAGCAACAGCGATGGTGAGAAGGCAACCAAAGTGCAGGACATCAAAAACAAC
CTGAAA

81 R S N S D G E K A T K V Q D I K N N L K

20

301

GAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTGCCCCCGTGGAGC
TGGCC

101 E A I E T I V A A M S N L V P P V E L A

25

WO 03/072014

PCT/US02/16877

361

AACCCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTGATGAACGTGCCTG
ACTTT

121 N P E N Q F R V D Y I L S V M N V P D F

5

421

GACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAAGGAG
TGCGT

141 D F P P E F Y E H A K A L W E D E G V R

10

481

GCCTGTCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGTGCCAGTACTTCCT
GGAC

161 A C Y E R S N E Y Q L I D C A Q Y F L D

15

541

AAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGATCAGGACCTGCTTC
GCTGC

181 K I D V I K Q A D Y V P S D Q D L L R C

20

601

CGTGTCTGACTTCTGGAATCTTTGAGACCAAGTTCAGGTGGACAAAGTCAACTT
CCAC

201 R V L T S G I F E T K F Q V D K V N F H

25

PCT/US02/16877

ATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGGATCCAGTGCTTCA
ACGAT

5

GTGACTGCCATCATCTTCGTGGTGGCCAGCAGCAGCTACAACATGGTCATCCGGG
AGGAC

10

AACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAGAGCATCTGGAACA
ACAGA

15

TGGCTGCGCACCATCTCTGTGATCCTGTTCTCAACAAGCAAGATCTGCTCGCTGA
GAAA

20

GTCTTGCTGGGAAATCGAAGATTGAGGACTACTTTCCAGAATTTGCTCGCTACAC
TACT

25

PCT/US02/16877

CTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTGACCCGGGCCAAGT
ACTTC

5

ATTCGAGATGAGTTTCTGAGGATCAGCACTGCCAGTGGAGATGGGCGTCACTACT
GCTAC

10

CCTCATTTCACCTGCGCTGTGGACACTGAGAACATCCGCCGTGTGTTCAACGACTG
CCGT

15

ClaI

GACATCATT CAGCGCATGCACCTTCGTCAGTACGAGCTGCTCATCGAT

20

SEQ ID NO.: 194

WO 03/072014

PCT/US02/16877

Human G q

XhoI

1

5 CTCGAGATGACTCTGGAGTCCATCATGGCGTGCTGCCTGAGCGAGGAGGCCAAGG
AAGCCC GGCGG

1 M T L E S I M A C C L S E E A K E A R R

61

10 ATCAACGACGAGATCGAGCGGCAGCTCCGCGAGGACAAGCGGGACGCCCCCGG
GAGCTC

21 I N D E I E R Q L R R D K R D A R R E L

121

15 AAGCTGCTGCTGCTCGGGACAGGAGAGAGTGGCAAGAGTACGTTTATCAAGCAGA
TGAGA

41 K L L L L G T G E S G K S T F I K Q M R

181

20 ATCATCCATGGGTCAGGATACTCTGATGAAGATAAAAGGGGCTTACCAAGCTGG
TGTAT

61 I I H G S G Y S D E D K R G F T K L V Y

PCT/US02/16877

CAGAACATCTTCACGGCCATGCAGGCCATGATCAGAGCCATGGACACACTCAAGA
TCCCA

81 Q N I F T A M Q A M I R A M D T L K I P

301

TACAAGTATGAGCACAAATAAGGCTCATGCACAATTAGTTCGAGAAGTTGATGTGG
AGAAG

101 Y K Y E H N K A H A Q L V R E V D V E K

10

361

GTGTCTGCTTTTGAGAATCCATATGTAGATGCAATAAAGAGTTTATGGAATGATCC
TGGA

121 V S A F E N P Y V D A I K S L W N D P G

15

421

ATCCAGGAATGCTATGATAGACGACGAGAATATCAATTATCTGACTCTACCAAAT
ACTAT

141 I Q E C Y D R R R E Y Q L S D S T K Y Y

20

481

CTTAATGACTTGGACCGCGTAGCTGACCCTGCCTACCTGCCTACGCAACAAGATGT
GCTT

161 L N D L D R V A D P A Y L P T Q Q D V L

25

PCT/US02/16877

AGAGTTCGAGTCCCCACCACAGGGATCATCGAATACCCCTTTGACTTACAAAGTG
TCATT

5

TTCAGAAATGGTCGATGTAGGGGGCCAAAGGTCAGAGAGAAGAAAATGGATACACT
GCTTT

10

GAAAATGTCACCTCTATCATGTTTCTAGTAGCGCTTAGTGAATATGATCAAGTTCT
CGTG

15

GAGTCAGACAATGAGAACCGAATGGAGGAAAGCAAGGCTCTCTTTAGAACAATTA
TCACA

20

TACCCCTGGTCCAGAACTCCTCGGTTATTCTGTTCTTAAACAAGAAAGATCTTCT
AGAG

25

WO 03/072014

PCT/US02/16877

841

GAGAAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAATATGATGGACCCC
AGAGA

281 E K I M Y S H L V D Y F P E Y D G P Q R

5

901

GATGCCCAGGCAGCCCCGAGAATTCATTCTGAAGATGTTCTGGACCTGAACCCAG
ACAGT

301 D A Q A A R E F I L K M F V D L N P D S

10

961

GACAAAATTATCTACTCCCACTTCACGTGCGCCACAGACACCGAGAATATCCGCT
TTGTC

321 D K I I Y S H F T C A T D T E N I R F V

15

C1aI

1021

TTTGTCGCCGTC AAGGACACCATCCTCCAGTTGAACCTGAAGGAGTACAATCTGG
TCATCGAT

20

341 F A A V K D T I L Q L N L K E Y N L V

25

SEQ ID NO.: 195

XhoI

1 M G C T V S A E D K A A A E R S K M I D

21 K N L R E D G E K A A R E V K L L L L G

41 A G E S G K S T I V K O M K I I H E D G

61 Y S E E E C R Q Y R A V V Y S N T I Q S

WO 03/072014

PCT/US02/16877

241

ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGCCGACCCCT
CCAGA

81 I M A I V K A M G N L Q I D F A D P S R

5

301

CGCGACGACGCCAGGCAGCTATTGCACTGTCCTGCACCGCCGAGGAGCAAGGCG
TGCTC

101 A D D A R Q L F A L S C T A E E Q G V L

10

361

CCTGATGACCTGTCCGGCGTCATCCGAGGCTCTGGGCTGACCATGGTGTGCAGG
CCTGC

121 P D D L S G V I R R L W A D H G V Q A C

15

421

TTTGCCCGCTCAAGGGAATACCAGCTCAACGACTCAGCTGCCTACTACCTGAACG
ACCTG

141 F G R S R E Y Q L N D S A A Y Y L N D L

20

481

GAGCGTATTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGCTACGGACCC
GCGTA

161 E R I A Q S D Y I P T Q Q D V L R T R V

25

WO 03/072014

PCT/US02/16877

541

AAGACCACGGGGATCGTGGAGACACACTTCACCTTCAAGGACCTACACTTCAAGA
TGTTT

181 K T T G I V E T H F T F K D L H F K M F

5

601

GATGTGGGTGGTCAGCGGTCTGAGCGGAAGAAGTGGATCCACTGCTTTGAGGGCG
TCACA

201 D V G G Q R S E R K K W I H C F E G V T

10

661

GCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGGTGCTAGCTGAGGACGA
GGAG

221 A I I F C V A L S A Y D L V L A E D E E

15

721

ATGAACCGCATGCATGAGAGCATGAAGCTATTCGATAGCATCTGCAACAACAAGT
GGTTC

241 M N R M H E S M K L F D S I C N N K W F

20

781

ACAGACACGTCCATCATCCTCTTCTCTCAACAAGAAGGACCTGTTTGAGGAGAAGA
TCACA

261 T D T S I I L F L N K K D L F E E K I T

25

WO 03/072014

PCT/US02/16877

841

CACAGTCCCCTGACCATCTGCTTCCTGAGTACACAGGGGCCAACAAATATGATG
AGGCA

281 H S P L T I C F P E Y T G A N K Y D E A

5

901

GCCAGTACATCCAGAGTAAGTTGAGGACCTGAATAAGCGCAAAGACACCAAGG
AGATC

301 A S Y I Q S K F E D L N K R K D T K E I

10

961

TACACGCACTTCACGTGCGCCACCGACACCAAGAACGTGCAGTTCGTGTTGACG
CCGTC

321 Y T H F T C A T D T K N V Q F V F D A V

15

ClaI

1021

ACCGATGTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTCATGCAT

341 T D V I I K N N L K D C G L F

20

SEQ ID NO.: 196

WO 03/072014

PCT/US02/16877

Human G 12/13

XhoI

1

5 CTCGAGATGTCCGGGGTGGTGC GGACCCTCAGCCGCTGCCTGCTGCCGGCCGAGG
CCGGCGGGGCC

1 M S G V V R T L S R C L L P A E A G G A

61

10 CGCGAGCGCAGGGCGGGCAGCGGCGCGCGACGCGGAGCGCGAGGCCCGGAGG
CGTAGC

21 R E R R A G S G A R D A E R E A R R R S

121

15 CGCGACATCGACGCGCTGCTGGCCCCGCGAGCGGCGCGGGTCCGGCGCCTGGTGA
AGATC

41 R D I D A L L A R E R R A V R R L V K I

181

20 CTGCTGCTGGGCGGGCGGAGAGCGGCAAGTCCACGTTCTCAAGCAGATGCGCA
TCATC

61 L L L G A G E S G K S T F L K Q M R I I

WO 03/072014

PCT/US02/16877

241

ACCGCCCGAGITTCGACCAGAAGGCGCTGCTGGAGTTCGCGACACCATCTTCG
ACAAC

81 H G R E F D Q K A L L E F R D T I F D N

5

301

ATCCTCAAGGGCTCAAGGGTTCTTGTTGATGCACGAGATAAGCTTGGCATTCTTG
GCAG

101 I L K G S R V L V D A R D K L G I P W Q

10

361

TATTCGAAAATGAGAAGCATGGGATGTTCTCTGATGGCCTTCGAGAACAAGGCGG
GGCTG

121 Y S E N E K H G M F L M A F E N K A G L

15

421

CCTGTGGAGCCGCCACCTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTCTGGA
GGGAT

141 P V E P A T F Q L Y V P A L S A L W R D

20

481

TCTGGCATCAGGGAGGCTTTCAGCCGGAGAAGCGAGTTTCAGCTGGGGGAGTCGG
TGAAG

161 S G I R E A F S R R S E F Q L G E S V K

25

WO 03/072014

PCT/US02/16877

541

TACTTCTGGACAACTTGGACCGGATCGGCCAGCTGAATTACTTTCCTAGTAAGCA
AGAT

181 Y F L D N L D R I G Q L N Y F P S K Q D

5

601

ATCCTGCTGGCTAGGAAAGCCACCAAGGGAATTGTGGAGCATGACTTCGTTATTA
AGAAG

201 I L L A R K A T K G I V E H D F V I K K

10

661

ATCCCTTTAAGATGGTGGATGTGGGCGGCCAGCGTCCCAGCGCCAGAAGTGGT
TCCAG

221 I P F K M V D V G G Q R S Q R Q K W F Q

15

721

TGCTTCGACGGGATCACGTCCATCCTGTTCATGGTCTCCTCCAGCAGTACGACCA
GGTC

241 C F D G I T S I L F M V S S S E Y D Q V

20

781

CTCATGGAGGACAGGCGCACCAACCGGCTGGTGGAGTCCATGAACATCTTCGAGA
CCATC

261 L M E D R R T N R L V E S M N I F E T I

25

WO 03/072014

PCT/US02/16877

841

GTCAACAACAAGCTCTTCTTCAACGTCTCCATCATTCTTCTCTCAACAAGATGGA
CCTC

281 V N N K L F F N V S I I L F L N K M D L

5

901

CTGGTGGAGAAGGTGAAGACCGTGAGCATCAAGAAGCACTTCCCGGACTTCAGGG
GCGAC

301 L V E K V K T V S I K K H F P D F R G D

10

961

CCGACACGCTGGAGGACGTCCAGCGCTACCTGGTCCAGTGCTTCGACAGGAAGA
GACGG

321 P H Q L E D V Q R Y L V Q C F D R K R R

15

1021

AACCGCAGCAAGCCACTCTTCCACCACTTCACCACCGCCATCGACACCGAGAACG
TCCGC

341 N R S K P L F H H F T T A I D T E N V R

20

1081

TTCGTGTTCCATGCTGTGAAAGACACCATCCTGCAGGAGAACCTGAAGGACATCA
TGCTG

361 F V F H A V K D T I L Q E N L K D I M L

25

WO 03/072014

PCT/US02/16877

ClaI

1141 CAGATCGAT

381 Q

5

10

SEQ ID NO.: 205

15

Human 2AR-ToxR (5-141) chimera stop GS1 -ToxR (5-141) chimera transcriptional
fusion

SalI +1 B2AR

20 1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC
TGGCACCCAA TGGAAGCCAT

WO 03/072014

PCT/US02/16877

61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT
GGGTGGTGGG CATGGGCATC

121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG
5 TGCTGGTCAT CACAGCCATT

181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA
TCACTTCACT GGCCTGTGCT

241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCCG
CCCATATTCT TATGAAAATG

10 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA
TTGATGTGCT GTGCGTCACG

361 GCCAGCATTG AGACCCTGTG CGTGATCGCA GTGGATCGCT
ACTTTGCCAT TACTTCAOCT

421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG
15 TGATCATTCT GATGGTGTGG

481 ATTTGTTCAG GCCTTAYCTC CTTCTTGCCC ATTCAAGTGC
ACTGGTACAG GGCCACCCAC

541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG
ACTTCTTCAC GAACCAAGCC

20 601 TATGCCATTG CCTCTTCCAT CGTGTCCCTC TACGTTCCCC
TGGTGATCAT GGTCTTCGTC

661 TACTCCAGGG TCITTCAGGA GGCCAAAAGG CAGCTCCAGA
AGATTGACAA ATCTGAGGGC

721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG
25 GGCGGACGGG GCATGGACTC

WO 03/072014

PCT/US02/16877

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC
TCAAGACGTT AGGCATCATC

841 ATGGGCACIT TCACCCTCTG CTGGCTGCCC TTCTTCATCG
TTAACATTGT GCATGTGATC

5 901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCCTCCTAA
ATTGGATAGG CTATGTCAAT

961 TCTGGTTTCA ATCCCCTTAT CTA CTACTGCCGG AGCCCA GATT
TCAGGATTGC CTTCCAGGAG

10 1021 CTTCTGTGCC TGCAGGTC TTC TTGAAG GCCTATGGCA
ATGGCTACTC CAGCAACGGC

1081 AACACAGGGG AGCAGAGTGG ATATCACTG GAACAGGAGA
AAGAAAATAA ACTGCTGTGT

1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG
GTACTGTGCC TAGCGATAAC

15

last B2AR linker

sequence

1201 ATTGATTAC AAGGGAGGAA TTGTAGTACA AATGACTCAC
TGCTAGAGCG TGGCCAGACG

20

PstI +5 toxR (5-141)

1261 GTCACCAACC TGCAGGACA CAACTCAAAA GAGATATCGA
TGAGTCATAT TGGTACTAAA

25

PCT/US02/16877

WO 03/072014

PCT/US02/16877

1981 CCATTGTGGC CGCCATGAGC AACCTGGTGC CCCCCGTGGA
GCTGGCCAAC CCCGAGAACC

2041 AGTTCAAGT GGACTACATC CTGAGTGTGA TGAACGTGCC
TGACTTTGAC TTCCCTCCCG

5 2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG
AGTGC GTGCC TGCTACGAAC

2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG CCCAGTACTT
CCTGGACAAG ATCGACGTGA

2221 TCAAGCAGGC TGACTATGTG CCGAGCGATC AGGACCTGCT
10 TCGCTGCCGT GTCCTGACTT

2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA
CTTCCACATG TTTGACGTGG

2341 GTGGCCAGCG CGATGAACGC CGCAAGTGG TCCAGTGCTT
CAACGATGTG ACTGCCATCA

15 2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG
GGAGGACAAC CAGACCAACC

2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGGAA
CAACAGATGG CTGCGCACCA

2521 TCTCTGTGAT CCTGTCCTC AACAAGCAAG ATCTGCTCGC
20 TGAGAAAGTC CTGTCTGGGA

2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA
CACTACTCCT GAGGATGCTA

2641 CTCCCAGGCC CGGAGAGGAC CCACGCGTGA CCCGGGCCAA
GTACTTCATT CGAGATGAGT

25 2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GGCCTCACTA
CTGCTACCCT CATTTCACCT

WO 03/072014

PCT/US02/16877

2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCACGA
TGCCCGTGAC ATCATTACGC

ClaI +5 toxR (5-141)

5 2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA
CAACTCAAAA GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT
10 TACCTTCGAT CCCCTAAGCA

2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTGC
ATTAGGCAGC AACGAAAGCC

3001 GAATTCTTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAAT
TTCTCGCAAT GATTGTCATG

15 3061 ACTTTGTTTG GCGAGAGCAA GGTTTGAAG TCGATGATTC
CAGCTTAACC CAAGCCATT

3121 CGACTCTGCG CAAAATGCTC AAAGATTGCA CAAAGTCCCC
ACAAACGTC AAAACGGTTC

3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGAACCGGT
20 TGAAGAAGAG ATGGCTCGCG

Stop XbaI

Stem-loop

3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG
25 ATCCCGCGC CCTCATCCGA

WO 03/072014

PCT/US02/16877

3301 AAGGGCG

5

SEQ ID NO.: 208

Vibrio cholerae Pctx::lacZ reporter fusion construct

10

XbaI

1 TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTACCGAT
AAAAACAGAA AATGATAAAA

3 ToxR binding repeats

15

61 AAGGACTAAA TAGTATATTT TGATTTTGA TTTTGAATT
CAAATAATAC AAATTTATTT

+1 lacZ

20

121 ACTTATTTAA TTGTTTTGAT CAATTATTTT TCTGTAAAC
AAAGGGAGCA TTATATGGTA

WO 03/072014

PCT/US02/16877

181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC
GTCGTGACTG GGAAAACCTT

241 GGC GTTACCC AACTTAATCG CCTTGCAGCA CATCCCCCTT
TCGCCAGCTG GCGTAATAGC

5 301 GAAGAGGCCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA
GCCTGAATGG CGAATGGCGC

361 TTTGCCTGGT TTCCGGCACC AGAAGCGGTG CCGGAAAGCT
GGCTGGAGTG CGATCTTCTT

421 GAGGCCGATA CTGTCGTCTG CCCCTCAAAC TGGCAGATGC
10 ACGGTACGA TCGCCTCATC

481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCCGT
TTGTTCCAC GGAGAATCCG

541 ACGGTTGTT ACTCGCTCAC ATTTAATGTT GATGAAAGCT
GGCTACAGGA AGGCCAGACG

15 601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT
GGTGCAACGG GCGCTGGGTC

661 GGTACGGCC AGGACAGTCG TTGCCGTCT GAATTGACC
TGAGCGCATT TTTACGCGCC

721 GGAGAAAACC GCCTCGCGGT GATGGTGCTG CGCTGGAGTG
20 ACGGCAGTTA TCTGGAAGAT

781 CAGGATATGT GCGGATGAG CGGCATTTTC CGTGACGTC
CGTTGCTGCA TAAACCGACT

841 ACACAAATCA GCGATTTCCA TGTTGCCACT CGCTTTAATG
ATGATTTTCA CCGCGCTGTA

25 901 CTGGAGGCTG AAGTTCAGAT GTGCGGCGAG TTGCGTGACT
ACCTACGGGT AACAGTTTCT

PCT/US02/16877

25 1681 TGCCCGATGT ACGCGCGCGT GGATGAAGAC CAGCCCTTCC
CGGCTGTGCC GAAATGGTCC

PCT/US02/16877

1801 CACGCGATGG GTAACAGTCT TGGCGGTTTC GCTAAATACT
GGCAGGCGTT TCGTCAGTAT

1921 GAAACGGCA ACCCGTGGTC GGCTTACGGC GGTGATTTTG
GCGATACGCC GAACGATCGC

2041 GCAAAACACC AGCAGCAGTT TTTCCAGTTC CGTTTATCCG
GGCAAACCAT CGAAGTGACC

2101 AGCGAATACC TGTTCCGTCA TAGCGATAAC GAGCTCCTGC
ACTGGATGGT GGCCTGGAT

2221 ATTGAAGTGC CTGAACTACC GCAGCCGGAG AGCGCCGGGC
AACTCTGGCT CACAGTACGC

2341 TGGCGTCTGG CGGAAAACCT CAGTGTGACG CTCCCCGCCG
CGTCCCACGC CATCCCGCAT

2401 CTGACCACCA GCGAAATGGA TTTTGCATC GAGCTGGGTA
ATAAGCGTTG GCAATTTAAC

146/268

WO 03/072014

PCT/US02/16877

2521 CTGCGCGATC AGTTCACCCG TGCACCGCTG GATAACGACA
TTGGCGTAAG TGAAGCGACC

2581 CGCATTGACC CTAACGCCTG GGTCGAACGC TGGAAGGCGG
CGGGCCATTA CCAGGCCGAA

5 2641 GCAGCGTTGT TGCAGTGCAC GGCAGATACA CTTGCTGATG
CGGTGCTGAT TACGACCGCT

2701 CACGCGTGGC AGCATCAGGG GAAAACCTTA TTTATCAGCC
GGAAAACCTA CCGGATTGAT

10 2761 GGTAGTGGTC AAATGGCGAT TACCGTTGAT GTTGAAGTGG
CGAGCGATAC ACCGCATCCG

2821 GCGCGGATTG GCCTGAACTG CCAGCTGGCG CAGGTAGCAG
AGCGGGTAAA CTGGCTCGGA

2881 TTAGGGCCGC AAGAAAATA TCCCGACCGC CTTACTGCCG
CTGTITTGA CCGCTGGGAT

15 2941 CTGCCATTGT CAGACATGTA TACCCGTAC GTCTTCCCGA
GCGAAAACGG TCTGCGCTGC

3001 GGGACGCGCG AATTGAATTA TGGCCACAC CAGTGGCGCG
GCGACTTCCA GTTCAACATC

3061 AGCCGCTACA GTCAACAGCA ACTGATGGAA ACCAGCCATC
20 GCCATCTGCT GCACGCGGAA

3121 GAAGGCACAT GGCTGAATAT CGACGGTTTC CATATGGGGA
TTGGTGCGCA CGACTCCTGG

3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC
GCTACCATTA CCAGTTGGTC

25

Stop Stem-loop XbaI

WO 03/072014

PCT/US02/16877

3241 TGGTGTCAAA AATAATAACGCCCTCAT CCGAAAGGGC GTCTAGA

SEQ ID NO.: 266

5

pMPX-74 MalE (1-28) fusion vector

SD old PstI +1

2401

10 GAATTCAGGCGCTTTT TAGACTGGTCGTAATGAAATTCAGGAGTTCTGCATATGA
AAAT

1

M K I

2461

15 AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI SalI XbaI

20

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

24

A L A K I I E A R L Q A S V D A E S R D

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PCT/US02/16877

FLAG

lost XbaI

2581 TTATAAAGATGACGATGACAAATAATAAGCTAGAGG

(transcriptional stop)

44 Y K D D D D K

5

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

10 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

15 SEQ ID NO.: 267

pMPX-75 MalE (1-28) fusion vector

SD old PstI +1

20 1621
CCATACCCGTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAAACAGG
TGAC

1

M K I K T G A

WO 03/072014

PCT/US02/16877

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

5 8 R I L A L S A L T T M M F S A S A L A K

Factor Xa PstI SalI XbaI
FLAG

1741

10 TCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCTAGAGATTATAAAGA
TGACG

Lost XbaI

1801 ATGACAAATAATAAGCTAGAGG (Transcriptional stop)

15

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 268

pMPX-88 MalE (1-28) fusion vector

5

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

1

M K I

10

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

15

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTGACGCCGAATCT
AGAGA

20

24

A L A K I I E A R L Q A S V D A E S R D

FLAG

lost XbaI

TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

WO 03/072014

PCT/US02/16877

44 Y K D D D D K

5 pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

10

SEQ ID NO.: 269

15 pMPX-93 MalE (1-28) fusion vector

SD old PstI +1

AGGAGGTTCTGCATATGAAAAT

20

1

M K I

WO 03/072014

PCT/US02/16877

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

5

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAGA

10 24 A L A K I I E A R L Q A S V D A E S R D

FLAG lost XbaI

TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

15 44 Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 270

pMPX-77 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

5 2401
GAATTCAGGCGCTTTTACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1 M K I

10 2461
AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4 K T G A R I L A L S A L T T M M F S A S

15 2521
GGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAA
GGCTA

24 A L A K I E E G K L V I W I N G D K G Y

20 2581
TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAAGATACCGGAATTAAAGTC
ACCGT

44 N G L A E V G K K F E K D T G I K V T V

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2641

TGAGCATCCGGATAAACTGGAAGAGAAATCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

5

2701

TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

10

2761

TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

15

2821

ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

20

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

25

WO 03/072014

PCT/US02/16877

2941

AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

5

3001

CTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

10

3061

CATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTTGA

204 I K D V G V D N A G A K A G L T F L V D

15

3121

CCTGATTA AAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

20

3181

TAATAAAGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

25

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3241

CAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

5

3301

GTTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

10

3361

AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

15

3421

ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

20

pMPX-72::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO Nsil-male (1-370 del 354-364)::FXa::PstI, SalI,

25 XbaI::FLAG-NheI insertion with Nsil & NheI and cloning into pMPX-72 cut with PstI &
XbaI.

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SEQ ID NO.: 271

5 pMPX-76 MalE (1-370 del 354-364) fusion vector

SD old PstI +1

1621

GCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAAACAGG

10 TGCAC

1

M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC

15 AAAA

8

R I L A L S A L T T M M F S A S A L A K

1741

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT

20 CGCTG

28

I E E G K L V I W I N G D K G Y N G L A

1801

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC

25 GGATA

PCT/US02/16877

48 E V G K K F E K D T G I K V T V E H P D

1861

AACTGGAAGAGAAATTTCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
5 CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
10 CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
15 CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGAT
20 CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101

25 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

WO 03/072014

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148 L P N P P K T W E E I P A L D K E L K A

2161

5 AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221

10 CTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281

15 GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341

20 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401

25 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

WO 03/072014

PCT/US02/16877

248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
5 CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAAGGTATTAACGCCGCGCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
10 CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
15 TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
20 CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

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2701

AAAACGCCCAGTCCGCTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

5

Sall XbaI FLAG Lost XbaI

2761

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
A(trxn stop)

10 368 V D A E S R D Y K D D D D K

pMPX-71::maIE(1-370 del 354-364)::FXa::PstI, Sall, XbaI::FLAG

Arabinose inducible, clone into PstI, Sall, XbaI

15 Made by cutting TOPO NsiI-maIE (1-370 del 354-364)::FXa::PstI, Sall,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI &
XbaI.

20

SEQ ID NO.: 272

pMPX-89 MaIE (1-370 del 354-364) fusion vector

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SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAAACAGGTGCAC

1 M K I K T G A

5

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

10

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

15

AAGTCGGTAAGAAAATTCGAGAAAGATACCGGAATTAAACTCACC GTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

20

AACTGGAAGAGAAAATTCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

25

WO 03/072014

PCT/US02/16877

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

5

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

10

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

15

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

20

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

25

PCT/US02/16877

5

10

15

20

25

268 Y G V T V L P T F K G Q P S K P F V G V

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PCT/US02/16877

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

5

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

10

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

15

Factor Xa PstI

AAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

20 348 E N A Q S A F W Y A V R I E A R L Q A S

Sall XbaI

FLAG

Lost XbaI

25 TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
(trxn stop)

WO 03/072014

PCT/US02/16877

368 V D A E S R D Y K D D D D K

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

5

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI &
XbaI.

10

SEQ ID NO.: 273

pMPX-94 MalE (1-370 del 354-364) fusion vector

15

SD old PstI +1

AGGAGGTTCTGCATATGAAAATAAAAAACAGGTGCAC

1

M K I K T G A

20

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTCCGCCTCGGCTCTCGCC
AAAA

8

R I L A L S A L T T M M F S A S A L A K

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PCT/US02/16877

TCGAAGAAGGTAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

5

AAGTCGGTAAGAAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GATA

48 E V G K K F E K D T G I K V T V E H P D

10

AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

15

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

20

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

25

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PCT/US02/16877

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

5

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

10

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

15

CTGCTGACGGGGTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

20

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

25

WO 03/072014

PCT/US02/16877

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

5

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

10

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

15

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

20

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

25

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PCT/US02/16877

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

5

Factor Xa PstI

AAAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

10 348 E N A Q S A F W Y A V R I E A R L Q A S

Sall XbaI FLAG Lost XbaI

TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG
15 (trxn stop)

368 V D A E S R D Y K D D D D K

pMPX-86::male(1-370 del 354-364)::FXa::PstI, Sall, XbaI::FLAG

20 Temperature inducible, clone into PstI, Sall, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, Sall,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI &
XbaI.

25

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SEQ ID NO.: 274

pMPX-79 TrxA (2-109 del 103-107) fusion vector

5

SD PstI SalI XbaI +2 trxA(del 103-107)

1

TAGCAGGAGGCCCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTA
TT

10

1

A S V D A E S R S D K I I

61

CACCTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
TCGTC

15

17

H L T D D S F D T D V L K A D G A I L V

121

GATTTCGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATG
AAATC

20

37

D F W A E W C G P C K M I A P I L D E I

181

GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGATCAAAACC
CTGGC

25

57

A D E Y Q G K L T V A K L N I D Q N P G

WO 03/072014

PCT/US02/16877

241

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

5 77 T A P K Y G I R G I P T L L L F K N G E

301

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

10 97 V A A T K V G A L S K G Q L K E N L A D

FLAG

Lost XbaI

15 361 TATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional
stop)

117 Y K D D D D K

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20 +1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 275

5 pMPX-78 TrxA (2-109 del 103-107) fusion vector

SD PstI

1
GAATTCAGGCGCTTTTGTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCT
10 C

1 A S

Sall XbaI +2 trxA(del 103-107)

61
15 GGTCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTT
GACAC

6 V D A E S R S D K I I H L T D D S F D T

121
20 GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTCTGGGCAGAGTGGTGC
GGTCC

26 D V L K A D G A I L V D F W A E W C G P

WO 03/072014

PCT/US02/16877

181

GTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAA
CTGAC

46 C K M I A P I L D E I A D E Y Q G K L T

5

241

CGTTGCAAAACTGAACATCGATCAAAACCTGGCACTGCGCCGAAATATGGCATC
CGTGG

66 V A K L N I D Q N P G T A P K Y G I R G

10

301

TATCCCGACTCTGCTGCTGTCAAAAACGGTGAAGTGGCGCAACCAAGTGGGT
GCACT

86 I P T L L L F K N G E V A A T K V G A L

15

FLAG

361

GTCTAAAGGTCAAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAA
TAATAA

20

106 S K G Q L K E N L A D Y K D D D D K

lost XbaI

GCTAGAGG (transcriptional stop)

25

pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

WO 03/072014

PCT/US02/16877

Rhamnose inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

- Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
5 insertion with PstI & NheI and cloning into pMPX-72 cut with PstI & XbaI.

SEQ ID NO.: 276

10

pMPX-90 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

- 15 AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT

1 A S V D A E S R S D K I I

- CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
20 TCGTC

17 H L T D D S F D T D V L K A D G A I L V

WO 03/072014

PCT/US02/16877

GATTTCGGGCAGAGTGGTGC GGTC CGTG CAAAATGATCGCCCCGATTCTGGATG
AAATC

37 D F W A E W C G P C K M I A P I L D E I

5

GCTGACGAATATCAGGGCAA ACTGACCGTTG CAAA ACTGAACATCGATCAAAACC
CTGGC

57 A D E Y Q G K L T V A K L N I D Q N P G

10

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

15

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

20

FLAG

Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

117 Y K D D D D K

25

WO 03/072014

PCT/US02/16877

pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

+1 Met required for protein to be fused

- 5 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
insertion with PstI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEQ ID NO.: 277

10

pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del 103-107)

- 15 AGGAGGTTCTGCAGGCCTCGGTCGACGCCGAATCTAGAAGCGATAAAAATTATT

1 A S V D A E S R S D K I I

- CACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCC
20 TCGTC

17 H L T D D S F D T D V L K A D G A I L V

PCT/US02/16877

5

10

15

ACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
GTGAA

77 T A P K Y G I R G I P T L L L F K N G E

GTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACTGG
CGGAT

97 V A A T K V G A L S K G Q L K E N L A D

20

FLAG

Lost XbaI

TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(transcriptional stop)

117 Y K D D D D K

25

WO 03/072014

PCT/US02/16877

pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI.

+1 Met required for protein to be fused

5 Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-NheI
insertion with PstI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

SEQ ID NO.: 278

10

pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

malE(1-28)

15

2401

GAATTCAGGCGCTTTTACTGCTGTAATGAAATTCAGGAGTTCTGCATATGA
AAAT

1

M K I

20

2461

AAAAACAGGTGCACGCATCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

WO 03/072014

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Factor Xa PstI SalI XbaI

2521

GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAAG

5 24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

2581

CGATAAAATTATTACCTGACTGACGACAGTTTTGACACGGATGTACTCAAAGCG
10 GACGG

44 D K I I H L T D D S F D T D V L K A D G

2641

GGCGATCCTCGTCGATTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
15 CCGAT

64 A I L V D F W A E W C G P C K M I A P I

2701

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAAC
20 ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

2761

TCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
25 CTGTT

WO 03/072014

PCT/US02/16877

104 Q N P G T A P K Y G I R G I P T L L L F

2821

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG

5 AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

FLAG

Lost XbaI

2881

10 GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG (trxn stop)

144 N L A D Y K D D D D K

pMPX-72::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

15

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

20

pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 malE (1-28)

WO 03/072014

PCT/US02/16877

1621

CCATACCCGTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAAACAGG
TGCAC

1

M K I K T G A

5

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8

R I L A L S A L T T M M F S A S A L A K

10

+2 trxA(2-109 del

Factor Xa PstI

SalI

XbaI

103-107)

1741

TCATCGAAGCCCGCTGCAGGCCTCGGTGCAGCCGAATCTAGAAGCGATAAAAT
TATTC

15

28

I I E A R L Q A S V D A E S R S D K I I

1801

ACCTGACTGACGACAGITTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCT
CGTCG

20

48

H L T D D S F D T D V L K A D G A I L V

1861

ATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGA
AATCG

25

68

D F W A E W C G P C K M I A P I L D E I

PCT/US02/16877

CTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCC
TGGCA

5 88 A D E Y Q G K L T V A K L N I D Q N P G

CTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTCAAAAACGGT
GAAG

10 108 T A P K Y G I R G I P T L L L F K N G E

TGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGC
GGATT

15 128 V A A T K V G A L S K G Q L K E N L A D

FLAG

2101 ATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional
stop)

20 148 Y K D D D D K

pMPX-71::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

WO 03/072014

PCT/US02/16877

Made by cutting TOPO Nsil-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

5 SEQ ID NO.: 280

pMPX-91 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

10 malE(1-28)

AGGAGGTTCTGCATATGAAAAAT

1

M K I

15

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

20

Factor Xa PstI SalI XbaI

GGCTCTCGCCAAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTCGACGCCGAATCT
AGAAG

24

A L A K I I E A R L Q A S V D A E S R S

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+2 trxA (2-109 del 103-107)

CGATAAAATTATTCACCTGACTGACGACAGTTTGTACACGGATGTACTCAAAGCG
5 GACGG

44 D K I I H L T D D S F D T D V L K A D G

GGCGATCCTCGTCGATTCTGCGGCAGAGTGGTGC GGTCCTGC AAAATGATCGCC
10 CCGAT

64 A I L V D F W A E W C G P C K M I A P I

TCTGGATGAAATCGCTGACGAATATCAGGGCAAAGTACC GTTGCA AAAACTGAAC
15 ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

TCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
20 CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
25 AAAGA

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124 K N G E V A A T K V G A L S K G Q L K E

FLAG

Lost XbaI

5 GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(trxn stop)

144 N L A D Y K D D D D K

pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

10 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

15

SEQ ID NO.: 281

pMPX-96 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

20

SD Lost PstI +1

malE(1-28)

AGGAGGTTCTGCATATGAAAAT

WO 03/072014

PCT/US02/16877

1

M K I

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
5 GCCTC

4 K T G A R I L A L S A L T T M M F S A S

Factor Xa PstI Sall XbaI

10 GGCTCTCGCCAAAATCATCGAAGCCCGCCTGCAGGCCTCGGTGACGCCGAATCT
AGAAAG

24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

15

CGATAAAATTATTCACCTGACTGACGACAGTTTGTGACACGGATGTACTCAAAGCG
GACGG

44 D K I I H L T D D S F D T D V L K A D G

20

GGCGATCCTCGTCGATTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCC
CCGAT

64 A I L V D F W A E W C G P C K M I A P I

WO 03/072014

PCT/US02/16877

TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTGC AAAACTGAAC
ATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

5

TCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTG
CTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

10

CAAAAACGGTGAAGTGGCGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTG
AAAGA

124 K N G E V A A T K V G A L S K G Q L K E

15

FLAG

Lost XbaI

GAACTGGCGGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC
(trxn stop)

20

144 N L A D Y K D D D D K

pMPX-86::malE(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

WO 03/072014

PCT/US02/16877

Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI
insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

5 SEQ ID NO.: 282

pMPX-83 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

10 malE(1-28)

2401

GAATTCAGGCGCTTTTACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGA
AAAT

1

M K I

15

2461

AAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCC
GCCTC

4

K T G A R I L A L S A L T T M M F S A S

20

2521

GGCTCTCGCCAAAATCGAAGAAGGTAACTGGTAATCTGGATTAACGGCGATAAA
GGCTA

24

A L A K I E E G K L V I W I N G D K G Y

25

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PCT/US02/16877

2581

TAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTC
ACCGT

44 N G L A E V G K K F E K D T G I K V T V

5

2641

TGAGCATCCGGATAAACTGGAAGAGAAAATCCCACAGGTTGCGGCAACTGGCGAT
GGCCC

64 E H P D K L E E K F P Q V A A T G D G P

10

2701

TGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGT
TGGC

84 D I I F W A H D R F G G Y A Q S G L L A

15

2761

TGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGAT
GCCGT

104 E I T P D K A F Q D K L Y P F T W D A V

20

2821

ACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGA
TTTA

124 R Y N G K L I A Y P I A V E A L S L I Y

25

WO 03/072014

PCT/US02/16877

2881

TAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTG
GATAA

144 N K D L L P N P P K T W E E I P A L D K

5

2941

AGAACTGAAAAGCGAAAAGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTAC
TTCAC

164 E L K A K G K S A L M F N L Q E P Y F T

10

3001

CTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAG
TACGA

184 W P L I A A D G G Y A F K Y E N G K Y D

15

3061

CATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTG
GTGA

204 I K D V G V D N A G A K A G L T F L V D

20

3121

CCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
GCCTT

224 L I K N K H M N A D T D Y S I A E A A F

25

WO 03/072014

PCT/US02/16877

3181

TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACAC

244 N K G E T A M T I N G P W A W S N I D T

5

3241

CAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCC
AAACC

264 S K V N Y G V T V L P T F K G Q P S K P

10

3301

GTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTG
GCGAA

284 F V G V L S A G I N A A S P N K E L A K

15

3361

AGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAA
GACAA

304 E F L E N Y L L T D E G L E A V N K D K

20

3421

ACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCA
CGTAT

324 P L G A V A L K S Y E E E L A K D P R I

25

WO 03/072014

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Factor Xa

3481

5 TGCCGCCACCATGGAAAACGCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAA
GCCCG

344 A A T M E N A Q S A F W Y A V R I E A R

PstI

SalI

XbaI +2 trxA (2-109 del 103-107)

3541

10 CCTGCAGGCCTCGGTGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACT
GACGA

364 L Q A S V D A E S R S D K I I H L T D D

3601

15 CAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTCTGG
GCAGA

384 S F D T D V L K A D G A I L V D F W A E

3661

20 GTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAA
TATCA

404 W C G P C K M I A P I L D E I A D E Y Q

3721

25 GGGCAAACTGACCGTTGCAAAACTGAACATCGATCAAAACCTGGCACTGCGCCG
AAATA

WO 03/072014

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424 G K L T V A K L N I D Q N P G T A P K Y

3781

TGCGATCCGTTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCA

5 ACCAA

444 G I R G I P T L L L F K N G E V A A T K

FLAG

10 3841

AGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGAT
GACGA

464 V G A L S K G Q L K E N L A D Y K D D D

15 3901 TGACAAATAATAAGCTAGAGG (transcriptional stop)

484 D K

pMPX-72::malE(1-320 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG,

20 Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI &
XbaI.

25

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 283

pMPX-82 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5

SD Lost PstI +1 malE (1-370 del

352-362)

1621

CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCATATGAAAATAAAACAGG

10 TGCAC

1

M K I K T G A

1681

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC

15 AAAA

8

R I L A L S A L T T M M F S A S A L A K

1741

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT

20 CGCTG

28

I E E G K L V I W I N G D K G Y N G L A

1801

AAGTCGGTAAGAAATTCGAGAAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC

25 GGATA

WO 03/072014

PCT/US02/16877

48 E V G K K F E K D T G I K V T V E H P D

1861

AACTGGAAGAGAAATTCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
5 CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

1921

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
10 CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

1981

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
15 CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

2041

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGAT
20 CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

2101

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAAGCTGA
25 AAGCGA

WO 03/072014

PCT/US02/16877

148 L P N P P K T W E E I P A L D K E L K A

2161

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
5 GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

2221

CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
10 CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

2281

GCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
15 AAACA

208 G V D N A G A K A G L T F L V D L I K N

2341

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGG
20 CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

2401

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
25 GAATT

WO 03/072014

PCT/US02/16877

248 T A M T I N G P W A W S N I D T S K V N

2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG

5 CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT

10 CGAAA

288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG

15 TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC

20 CATGG

328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

WO 03/072014

PCT/US02/16877

2701

AAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

348 E N A Q S A F W Y A V R I E A R L Q A S

5

SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTGA
CACGG

10 368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTCTGGGCAGAGTGGTGCGG
TCCGT

15 388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC
TACCG

20 408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAACTGAACATCGATCAAAACCTGGCACTGCGCCGAAATATGGCATCCG
TGTA

25 428 V A K L N I D Q N P G T A P K Y G I R G

WO 03/072014

PCT/US02/16877

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC
ACTGT

5 448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
10 ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGG (transcriptional stop)

15

pMPX-71::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG

Arabinose inducible, clone into PstI, SalI, XbaI

20

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI &
XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 284

pMPX-92 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5

SD Lost PstI +1 malE (1-370 del
354-364)

AGGAGGTTCTGCATATGAAAATAAAAACAGGTGCAC

10

1

M K I K T G A

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

15

8

R I L A L S A L T T M M F S A S A L A K

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

20

28

I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

25

48

E V G K K F E K D T G I K V T V E H P D

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PCT/US02/16877

AACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

5 68 K L E E K F P Q V A A T G D G P D I I F

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

10 88 W A H D R F G G Y A Q S G L L A E I T P

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

15 108 D K A F Q D K L Y P F T W D A V R Y N G

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGAT
CTGC

20 128 K L I A Y P I A V E A L S L I Y N K D L

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

25 148 L P N P P K T W E E I P A L D K E L K A

WO 03/072014

PCT/US02/16877

AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

5 168 K G K S A L M F N L Q E P Y F T W P L I

CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

10 188 A A D G G Y A F K Y E N G K Y D I K D V

CGGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCTCGTTGACCTGATTAA
AACA

15 208 G V D N A G A K A G L T F L V D L I K N

2341

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTAATAAAGG
CGAAA

20 228 K H M N A D T D Y S I A E A A F N K G E

2401

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

25 248 T A M T I N G P W A W S N I D T S K V N

WO 03/072014

PCT/US02/16877

2461

ATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG
CGTGC

5 268 Y G V T V L P T F K G Q P S K P F V G V

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

10 288 L S A G I N A A S P N K E L A K E F L E

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

15 308 N Y L L T D E G L E A V N K D K P L G A

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

20 328 V A L K S Y E E E L A K D P R I A A T M

Factor Xa PstI

2701

AAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
25 CTCGG

WO 03/072014

PCT/US02/16877

348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI +2 trxA (2-109 del 103-107)

2761

5 TCGACGCCGAATCTAGAAAGCGATAAAATTATTCACCTGACTGACGACAGTTTGA
CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

10 ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCGGGCAGAGTGGTGCGG
TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

15 GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC
GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

20 TTGCAAAACTGAACATCGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCG
TGTA

428 V A K L N I D Q N P G T A P K Y G I R G

WO 03/072014

PCT/US02/16877

3001

TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCCAACCAAAGTGGGTGC
ACTGT

448 I P T L L L F K N G E V A A T K V G A L

5

FLAG

3061

CTAAAGGTCAAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATA
ATAAG

10

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

CTAGAGGTACC (transcriptional stop)

15

pMPX-84::maIE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-maIE (1-370 del 354-364)::FXa::PstI, SalI,

20

XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI &
XbaI.

WO 03/072014

PCT/US02/16877

SEQ ID NO.: 285

pMPX-97 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

5 SD Lost PstI +1 male (1-370 del
354-364)

AGGAGGTTCTGCATATGAAAAATAAAACAGGTGCAC

1 M K I K T G A

10

GCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCC
AAAA

8 R I L A L S A L T T M M F S A S A L A K

15

TCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCT
CGCTG

28 I E E G K L V I W I N G D K G Y N G L A

20

AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCC
GGATA

48 E V G K K F E K D T G I K V T V E H P D

25

WO 03/072014

PCT/US02/16877

AACTGGAAGAGAAATTCACAGGTGCGGCAACTGGCGATGGCCCTGACATTAT
CTTCT

68 K L E E K F P Q V A A T G D G P D I I F

5

GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCAC
CCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

10

ACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAA
CGGCA

108 D K A F Q D K L Y P F T W D A V R Y N G

15

AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAAGAT
CTGC

128 K L I A Y P I A V E A L S L I Y N K D L

20

TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGA
AAGCGA

148 L P N P P K T W E E I P A L D K E L K A

25

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AAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT
GATTG

168 K G K S A L M F N L Q E P Y F T W P L I

5

CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGA
CGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

10

GCGTGGATAACGCTGGCGGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAA
AAACA

208 G V D N A G A K A G L T F L V D L I K N

15

2341

AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCITTAATAAAGG
CGAAA

228 K H M N A D T D Y S I A E A A F N K G E

20

2401

CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGT
GAATT

248 T A M T I N G P W A W S N I D T S K V N

25

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2461

ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTGG
CGTGC

268 Y G V T V L P T F K G Q P S K P F V G V

5

2521

TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCCT
CGAAA

288 L S A G I N A A S P N K E L A K E F L E

10

2581

ACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGG
TGCCG

308 N Y L L T D E G L E A V N K D K P L G A

15

2641

TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCAC
CATGG

328 V A L K S Y E E E L A K D P R I A A T M

20

Factor Xa PstI

2701

AAAACGCCCAGTCCGCTTCTGGTATGCCGTGCGTATCGAAGCCCGCCTGCAGGC
CTCGG

25

348 E N A Q S A F W Y A V R I E A R L Q A S

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SalI XbaI +2 trxA (2-109 del 103-107)

2761

TCGACGCCGAATCTAGAAGCGATAAAATTATTCACCTGACTGACGACAGTTTGA

5 CACGG

368 V D A E S R S D K I I H L T D D S F D T

2821

ATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTCTGGGCAGAGTGGTGCGG

10 TCCGT

388 D V L K A D G A I L V D F W A E W C G P

2881

GCAAAATGATCGCCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAAC

15 GACCG

408 C K M I A P I L D E I A D E Y Q G K L T

2941

TTGCAAACTGAACATCGATCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCG

20 TGGTA

428 V A K L N I D Q N P G T A P K Y G I R G

3001

TCCCAGCTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGC

25 ACTGT

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448 I P T L L L F K N G E V A A T K V G A L

FLAG

3061

5 CTAAAGGTCAGTTGAAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAAATA
ATAAG

468 S K G Q L K E N L A D Y K D D D D K

Lost XbaI

10 CTAGAGGTACC (transcriptional stop)

pMPX-86::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

15

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI &
XbaI.

20

SEQ ID NO.: 151

pMPX-66 arabinose-inducible expression vector

25 1 TC3GCGCTTT CGGTGATGAC GGTGAAACC TCTGACACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGCTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG

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121 TTGGCGGGTG TCGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
5 241 ATTCCGCATT CAGGCTGCGC AACTGTTGGG AAGGCGGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGCGGATT AAGTTGGGTA
ACGCCAGGGT

10 361 TTTCCAGTC ACGACGTTGT AAAACGACGG CAGTGCCAA GCTTCAAGCC
GTCAATTGTC

15 421 TGATTCGGTTA CCAATTATGA CAACTTGACG GCTACATCAT TCACTTTTTTC
TTCACAAACCG

20 481 GCACGGAAC TCGTCGGGCT GGCCCCGGTG CATTTTTTAA ATACCCGCGA
GAAATAGAGT
541 TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAA
601 AGCAGCTTCG CTTGGCTGAT ACGTTGGTCC TCGCGCCAGC TTAAGACGCT
AATCCCTAAC

25 661 TGCTGGCGGA AAAGATGTGA CAGACGCGAC GCGACAAAGC AAACATGCTG
TGCGACGCTG
721 GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAGC
CTCGCGTACC
781 CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCATGCGCCG
CAGTAACAT

30 841 TGCTCAAGCA GATTTATCGC CAGCAGCTCC GAATAGCGCC CTTCCTCCCTG
CCCGGCGTTA
901 ATGATTGTC CAAACAGGTC GCTGAAATGC GGCTGGTGGC CTTCATCCGG
GCGAAGAAC

35 961 CCCGTATTGG CAAATATTGA CGGCCAGTTA AGCCATTTCAT GCCAGTAGGC
GCGCGGACGA
1021 AAGTAAACCC ACTGGTGATA CCATTCGCGA GCCTCCGGAT GACGACCGTA
GTGATGAATC
1081 TCTCCTGGCG GGAACAGCAA AATATCACCC GGTCGGCAA CAAATTCCTG
TCCCTGATTT

40 1141 TTCACACCC CTTGACCGCG AATGGTGAGA TTGAGAATAT AACCTTTCAT
TCCAGCGGT
1201 CGGTGATATA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAACC
CGCCACCAGA

45 1261 TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCAITTT GCGCTTCAGC
CATACTTTTC

50 1321 ATACTCCGCG CATTCAGAGA AGAAACCAAT TGTCCATATT GCATCAGACA
TTGCCGTAC

55 1381 TCGCTCTTTT ACTGGCTCTT CTCGCTAACC AAACCGGTAA CCCCGCTTAT
TAAAAGCAIT
1441 CTGTAAACAAA GCGGGACCAA AGCCATGACA AAAACCGSTA ACAAAGTGT
CTATAATCAC
1501 GGCAGAAAAA TCCACATTGA TTATTGTCAC GCGTCACAC TTTGCTATGC
CATAGCATTT
1561 TTATCCATAA GATTAGCGGA TCCTACCTGA CGCTTTTTCAT CGCAACTCTC
TACTGTTTCT

60

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3241 TCATTGAGCT CCGGTTCCCA ACGATCAAGG CGAGTACAT GATCCCCCAT
GTTGTGCAAA
3301 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTACAGAA GTAAGTTGGC
5 CGCAGTGTGA
3361 TCACCTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC
CGTAAGATGC
3421 TTTTCTGTGA CTGGTGAGTA CTCACCAAG TCATCTGAG AATAGTGTAT
GCGCGACCG
3481 AGTTGCTCTT GCCCGGCGTC AATACGGAT AATACCGCG CACATAGCAG
10 AACTTTAAAA
3541 GTGCTCATCA TTGGAACG TTCCTCGGG CGAAAACTC CAAGGATCCT
ACCGCTGTTG
3601 AGATCCAGTT CGATGTAACC CACTCGTGCA CCAACTGAT CTTAGCATC
TTTACTTTC
15 3661 ACCAGCGTTT CTGGTGAGC AAAACAGGA AGGCAAAATG CCGCAAAAA
GGGAATAAGG
3721 GCGACACGGA AATGTTGAAT ACTCATACTC TTCCTTTTC AATATTATTG
AAGCATTTAT
3781 CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAA
20 TAAACAAATA
3841 GGGGTTCCGC GCACATTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
CATATTATTC
3901 ATGACATTAA CTTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC
25 The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified
aligned Shine-Delgarno (SD) sequence with SalI followed by XbaI, a stem-loop transcriptional
stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

30 SEQ ID NO.: 152

pMPX-72 rhamnose-inducible expression vector

1 TCGCGGTTT CGGTGATGAC GGTGAAAC TCAGACAT GCAGCTCCCG
35 GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAGCCCG TCAGGGCGCG
TCAGCGGGTG
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
40 181 ACCATATGCG GTGTGAAATA CCGCACAGAT CGGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTGCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
TCTTCGCTAT
301 TACGCCAGCT GCGAAAGGG GAGTGTGCTG CAAGGCGATT AAGTTGGGTA
45 ACGCCAGGGT

361 TTTCCAGTC ACGACGTGT AAAACGACGG CCAGTGCCAA GCTTAATTAA
TCTTTCGCG
50 Stop rhaR
HindIII
421 AATTGAGATG ACGCCACTGG CTGGGCGTCA TCCCAGTTTC CCGGTAAC
ACCACGAAA
481 AATAGTACT ATCTTCAAAG CCACATTCGG TCGAAATATC ACTGATTAC
55 AGCGGCTAT
541 GCTGGAGAAG ATATTGCGCA TGACACACTC TGACCTGTCG CAGATATGTA
TGATGGTCA

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601 TTCCAGTCTG CTGGCGAAAT TGCTGACGCA AAACGCGCTC ACTGCACGAT
GCCTCATCAC
661 AAAATTTTATC CAGCGCAAAG GGACTTTTCA GGCTAGCCGC CAGCCGGGTA
ATCAGCTTAT
5 721 CCAGCAACGT TTCGCTGGAT GTTGGCGGCA ACGAATCACT GGTGTAACGA
TGGCGATTCA
781 GCAACATCAC CAACTGCCCG AACAGCAACT CAGCCATTTT GTTAGCAAAAC
GGCACATGCT
841 GACTACTTTC ATGCTCAAGC TGACCGATAA CCTGCCGCGC CTGCGCCATC
10 CCCATGCTAC
901 CTAAGCGCCA GTGTGGTTGC CCTGCGCTGG CGTTAAATCC CGGAATCGCC
CCCTGCCAGT
961 CAAGATTTCAG CTTCAGACGC TCCGGGCAAT AAATAATAAT CTGCAAAACC
AGATCGTTAA
15 1021 CGGAAGCGTA GGAGTGTTTA TCGTCAGCAT GAATGTAAAA GAGATCGCCA
CGGGTAATGC
1081 GATAAGGGCG ATCGTTGAGT ACATGCAGGC CATTACCGCG CAGACAAATC
ACCAAGCTCAC
1141 AAAAATCATG TGTATGTTCA GCAAAGACAT CTTGCGGATA ACGGTGAGCC
20 ACAGCGACTG
1201 CCTGCTGGTC GCTGGCAAAA AAATCATCTT TGAGAAGTTT TAACTGATGC
GCCACCGTGG
1261 CTACCTCGGC CAGAGAACGA AGTTGATTAT TCGCAATATG GCGTACAAAT
ACGTTGAGAA
25
Stop rhaS Start rhaR
1321 GATTTCGCGT TT ATTGCAGAAA GCCATCCCGT CCCTGGCGAA TATCACGCGG
TGACCAGTTA
<--
30
1381 AACTCTCGGC GAAAAAGCGT CGAAAAAGTGG TTAATGTCGC TGAATCCACA
GCGATAGGCG
1441 ATGTCAGTAA CGCTGGCCTC GCTGTGGCGT AGCAGATGTC GGGCTTTCAT
CAGTCGAGG
35 1501 CGGTTACAGT ATCGCTGAGG CGTCAGTCCC GTTTGCTGCT TAAGCTGCCG
ATGTAGCGTA
1561 CGCAGTGAAA GAGAAAAATTG ATCCGCCACG GCATCCCAAT TCACCTCATC
GGCAAAATGG
40 1621 TCTCCAGCC AGGCCAGAAG CAAGTTGAGA CGTGATGCGC TGTTTTCCAG
GTTCTCCTGC
1681 AAACCTGCTTT TACGCAGCAA GAGCAGTAAT TGCATAAACA AGATCTCGCG
ACTGGCGGTC
1741 GAGGGTAAAT CATTTCCTCC TTCTGCTGTG TCCATCTGTG CAACCAAGCTG
TCGCACCTGC
45 1801 TGCAATACGC TGTGTTTAA CCGCCAGTGA GACGGATACT GCCCATCCAG
CTCTGTGTGC
1861 AGCAACTGAT TCAGCCCGGC GAGAAACTGA AATCGATCCG GCGAGCGATA
CAGCACATTG
1921 GTCAGACACA GATTATCGGT ATGTTTCATAC AGATGCCGAT CATGATCGCG
50 TACGAAACAG
1981 ACCGTGCCAC CGGTGATGGT ATAGGGCTGC CCAATTAACA CATGAATACC
CGTGCCATGT
2041 TCGACAATCA CAATTTCATG AAAATCATGA TGATGTTTCA GAAAAATCCGC
CTGCGGGAGC
55 2101 CGGGGTCTTA TCGCCACGGA CGCGTTACCA GACGGAAAAA AATCCACACT
ATGTAAATAG
Start rhaS
2161 GTCATACTGCG CCTCCTGATG TCGTCAACAC GCGGAAATAG TAATCACGAG
60 GTCAGGTTCT

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<--

2221 TACCTTAAAT TTTCGACGGA AAACCACGTA AAAACGTCG ATTTTTCAGG
ATACAGCGTG
5 2281 AATTTTTCAGG AAATGCGGTG AGCATCACAT CACCACAATT CAGCAAAATG
TGAACATCAT
2341 CACGTTTCATC TTTCCTTGGT TGCCAAATGGC CCATTTTCTCT GTCACTAAGC
AGAAGGTGCG

10 2401 GAATTCAGGC GCTTTTGTAGA CTGGTCGTAA TGAAATTCAG GAGGTTCTGC
AGGTCGACTC SD PstI SalI

XbaI Stem-loop KpnI
15 2461 TAGAGGATCC CCGCGCCCTC ATCCGAAAGG CGGTATTGGT ACCGAGCTCG
AATTCGTAAT

2521 CATGGTCATA GCTGTTTCTT GTGTGAAAT GTTATCCGCT CACAATTCGA
CACAACATAC
20 2581 GAGCCGGAAG CATAAAGTGT AAAGCCTGGG GTGCCAATG AGTGAGCTAA
CTCACATTAA
2641 TTGCGTTGCG CTCACGTGCC GCTTTCAGT CGGGAACCT GTCTGCCCAG
CTGCATTAAT

2701 GAATCGGCCA ACGCGCGGG AGAGGCGGT TGCGTATTGG GCGCTCTTCC
GCTTCTCTCG
25 2761 TCACTGACTC GCTGCGCTCG GTCGTTCCGC TCGCGCGAGC GGTATCAGCT
CACTCAAGG
2821 CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAGAACAATG
TGAGCAAAAG

30 2881 GCCAGCAAAA GGCCAGGAAC CGTAAAAGG CCGCGTTGCT GCGGTTTTTC
CATAGGCTCC
2941 GCCCCCCTGA CGAGCATCAC AAAAATCGAG GCTCAAGTCA GAGGTGGCGA
AACCGACAG

3001 GACTATAAAG ATACCAGCGG TTTCCCCCTG GAAGCTCCCT GGTGCGCTCT
CCTGTTCCGA
35 3061 CCTGCGCGCT TACCGGATAC CTGTCCGCTT TTCTCCCTTC GGAAGCGTG
GCGCTTTCTC
3121 ATAGCTCAGC CTGTAGGTAT CTCAGTTCGG TGTAGGTCTG TCGCTCCAAG
CTGGGCTGTG

3181 TGCACGAACC CCGCGTTTCA CCGACCGCT GCGCCTTATC CGGTAACAT
CGTCTTGAGT
40 3241 CCAACCCGGT AAGACACGAC TTATGCCAC TGGCAGCAGC CACTGTTAAC
AGGATTAGCA
3301 GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC
TACGGCTACA

45 3361 CTAGAAGGAC AGTATTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC
GGAAAAGAG
3421 TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT
TTTGTTTGCA

3481 AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAGAAGA TCCTTTGATC
TTTCTTACGG
50 3541 GGTCTGACGC TCAGTGGAAC GAAACTCAC GTTAAGGGAT TTTGGTCATG
AGATTATCAA
3601 AAAGGATCTT CACCTAGATC CTTTTAAAT AAAAATGAAG TTTTAAATCA
ATCTAAAGTA

55 3661 TATATGAGTA AACTTGTGCT GACAGTTACC AATGCTTAAT CAGTGAGGCA
CCTATCTCAG
3721 CGATCTGTCT ATTTGTTTCA TCCATAGTTG CCGTACTCCC GTCGTGTAG
ATAACTACGA

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3781 TACGGGAGGG CITACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAC
CCACGCTCAC
3841 CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG GGCCGAGCGC
AGAAGTGGTG
5 3901 CTGCAACTTT ATCCGCCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT
AGAGTAAAGTA
3961 GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC TACAGGCATC
GTGGTGTACAC
10 4021 GCTCGTCGTT TGGTATGGCT TCATTAGCTC CCGGTTCCCA ACGATCAAGG
CGAGTTACAT
4081 GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GTCCTTCGG TCTTCGGATC
GTGTGTCAGAA
4141 GTAAGTTGGC CGCAGTGTTA TCATCTATGG TTATGGCAGC ACTGCATAT
TCTCTTACTG
15 4201 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG
TCATTCTGAG
4261 AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGGCTC AATACGGGAT
AATACCGCGC
20 4321 CACATAGCAG AACTTTAAAA GTGCTCATCA TTGAAAAACG TTCTTCGGGG
CGAAAACCTCT
4381 CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAAAC CACTCGTGCA
CCCAACTGAT
4441 CTTCAGCATC TTITACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA
AGGCMAATG
25 4501 CCGCAAAAAA GGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC
TTCTTTTTTC
4561 AATATTATTG AAGCATTATC CAGGGTTATT GTCTCATGAG CGGATACATA
TTTGAATGTA
4621 TTTAGAAAAA TAAACAAATA GGGGTTCGCG GCACATTTC CCGAAAAGTG
30 CCACTTGACG
4681 TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC
ACGAGGCCCT
4741 TTCGTC

The segment rhaR through Priha was taken from the E. coli chromosome using PCR added
HindIII and modified aligned Shine-Delgarno (SD) sequence with PstI followed by SalI, XbaI, a
stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18
using HindIII and KpnI.

40

SEQ ID NO.: 153

pMPX-67 rhamnose-inducible expression vector

45 1 TCGCGCGTTT CGGTGATGAC GGTGAAACC TCTGACACAT GCAGCTCCCC
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGGAT GCGGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
50 121 TTGGCGGGTG TCGGGGCTGG CTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCAGAGAT GCGTAAGGAG AAAATACCGC
ATCAGGCGCC
241 ATTGCGCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC
55 TCTTCGCTAT
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGGCGATT AAGTTGGGTA
ACGCCAGGGT

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361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCAA GCTTAATTAA
TCTTTCGCG

HindIII

5 421 AATTGAGATG ACGCCACTGG CTGGGGTGCA TCCCAGTTTC CCGGTAAC
ACCACGAAA
481 AATAGTTACT ATCTTCAAAG CCACATTCGG TCGAATATC ACTGATTAA
AGGCGGCTAT

10 541 GCTGGAGAAG ATATTGCGCA TGACACACTC TGACCTGTC CAGATATTGA
TTGATGGTCA
601 TTCCAGTCTG CTGGCGAAAT TGCTGACGCA AAACGCGCTC ACTGCACGAT
GCCTCATCAC
661 AAAATTTATC CAGCGCAAAG GGACTTTTCA GGCTAGCCGC CAGCCGGGTA
ATCAGCTTAT

15 721 CCAGCAACGT TTCGCTGGAT GTTGGGGGCA ACGAATCACT GGTGTAAACGA
TGGCGATTCA
781 GCAACATCAC CAACTGCCCG AACAGCAACT CAGCCATTTT GTTAGCAAA
GGCACATGCT

20 841 GACTACTTTC ATGCTCAAGC TGACCGATAA CCTGCCGCGC CTGCGCCATC
CCCATGCTAC
901 CTAAGCGCCA GTGTGGTTGC CCTGCGCTGG CGTTAAATCC CGGAATCGCC
CCCTGCCAGT

25 961 CRAAGATTCAG CTTCAGACGC TCCGGGCAAT AAATAATATT CTGCAAAACC
AGATCGTTAA
1021 CGAAGCGTA GGAGTGTTTA TCGTCAGCAT GAATGTAAA GAGATCGCCA
CGGGTAATGC
1081 GATAAGGGCG ATCGTTGAGT ACATGCAGGC CATTACCGCG CAGACAATC
ACCAGCTCAC

30 1141 AAAAATCATG TGTATGTTCA GCAAAGACAT CTTCGGGATA ACGSTCAGCC
ACAGCGACTG
1201 CTTGCTGGTC GCTGGCAAAA AAATCATCTT TGAGAAGTTT TAACTGATGC
GCCACCGTGG
1261 CTACCTCGGC CAGAGAACGA AGTTGATTAT TCGCAATATG GCGTACAAAT

35 ACGTTGAGAA

Stop rhaS Start rhaR

1321 GATTGCGGTT ATTGCAGAAA GCCATCCCCG CCCTGGCGAA TATCACGCGG
TGACCAGTTA

40 <--

1381 AACTCTCGGC GAAAAAGCGT CGAAAAGTGG TTACTGTGCG TGAATCCACA
GCGATAGGCG
1441 ATGTCAAGTAA CGCTGGCCTC GCTGTGGCGT AGCAGATGTC GGGCTTTCAT
CAGTCGCAGG

45 1501 CGGTTTCAGT ATCGTGAGG CGTCAGTCCC GTTTGCTGCT TAAGCTGCCG
ATGTAGCGTA
1561 CGCAGTGAAA GAGAAAAATTG ATCCGCCACG GCATCCCAAT TCACCTCATC
GGCAAAATGG

50 1621 TCCTCCAGCC AGGCCAGAAG CAAGTTGAGA CGTGATGCGC TGTTTTCCAG
GTTCTCCTGC
1681 AAACCTGCTTT TACGCAGCAA GAGCAGTAAT TGCATAAACA AGATCTCGCG
ACTGGCGGTC

55 1741 GAGGGTAAAT CATTTTCCCC TTCTTGCTGT TCCATCTGTG CAACCAGCTG
TCGCACCTGC
1801 TGCAATACGC TGTGGTTAAC GCGCCAGTGA GACGATACT GCCATCCAG
CTCTGTGGC
1861 AGCAACTGAT TCAGCCCGGC GAGAACTGA AATCGATCCG GCGAGCGATA
CAGCACATTG

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1921   GTCAGACACA GATTATCGGT ATGTTTCATAC AGATGCCGAT CATGATCGCG
TACGAAACAG
1981   ACCGTGCCAC CGGTGATGGT ATAGGGCTGC CCATTAAACA CATGAATACC
CGTGCCATGT
5      2041   TCGACAATCA CAATTTTCATG AAAATCATGA TGATGTTTCAG GAAATCCGCG
CTCGGGAGGC
2101   CGGGGTTCTA TCGCCACGGA CGCGTTACCA GACGGAAAAA AATCCCACT
ATGTAATACG

10      start rhaS
2161   GTCATACTGG CCTCTGATG TCGTCAACAC GCGGAAATAG TAATCACGAG
GTCAGGTTCT
      <--

15      2221   TACCTTAAAT TTTCGACGGA AAACACGTA AAAACGTCG ATTTTTCAG
ATACAGCGTG
2281   AATTTTCAGG AAATGCGGTG AGCATCACAT CACCACAATT CAGCAAATTG
TGAACATCAT
2341   CACGTTTCATC TTTCCTGGT TGCCAATGCG CCATTTTCCT GTCACTAACG
20      AGAAGGTCGC

                                           SD      SalI      XbaI

2401   GAATTCAGGC GCTTTTTAGA CTGGTCGTAA TGAAATTCAG GAGGTGTGCG
25      ACTCTAGAGG

                               Stem-loop           KpnI
2461   ATCCCCGCGCG CCTCATCCGA AAGGGCGTAT TGGTACCGAG CTGGAATTGC
TAATCATGGT

30

2521   CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT TCCACACAAC
ATACGAGCCG
2581   GAAGCATAAA GTGTAAAGCC TGGGGTGCTT AATGAGTGAG CTAACTCACA
TTAATTGCGT
35      2641   TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT
TAATGAATCG
2701   GCCAACGCGC GGGGAGAGGC GGTTTGCGTA TTGGGCGCTC TTCCGCTTCC
TCGCTCACTG
40      2761   ACTCGCTGCG CTCGTCGTT CGGCTGCGGC GAGCGGTATC AGCTCACTCA
AAGCGCGTAA
2821   TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA
AAGAGCCAGC
2881   AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG
CTCCGCCCCC
45      2941   CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
ACAGGACTAT
3001   AAAGATACCA GCGTTTCCC CCTGGAAGCT CCCTCGTGGC CTCTCCTGTT
CCGACCCTGC
50      3061   CGCTTACCGG ATACCTGTCC GCCTTTCTCC CTTCGGGAAG GGTGGCGCTT
TCTCATAGCT
3121   CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTTCGCTC CAAGCTGGGC
TGTTGTGACG
3181   AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT
55      GAGTCCAACC
3241   CGGTAAAGACA OGAATTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
AGCAGAGCGA
3301   GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC
TACACTAGAA

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3361  GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCCGAAAA
AGAGTTTGGTA
3421  GCTCTTGATC CGGCAACAA ACCACGCTG GTAGCGGTGG TTTTITTTGTT
TGCAAGCAGC
5    3481  AGATTACGCG CAGAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
ACGGGGTCTG
3541  ACGCTCAGTG GAACGAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA
TCAAAAAGGA
3601  TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTAA ATCAATCTAA
10  AGTATATATG
3661  AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC
TCAGCGATCT
3721  GTCTATTTCG TTCATCCATA GTTGCTGAC TCCCGCTGT GTAGATAACT
ACGATACGGG
15  3781  AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC
TCACCGGCTC
3841  CAGATTATTC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
GGTCCGCAA
3901  CTTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGGA AGCTAGAGTA
20  AGTAGTTCGC
3961  CAGTTAATAG TTGCGCAAC GTTGTGCCA TTGCTACAGG CATCGTGGTG
TCACGCTCGT
4021  CGTTTGGTAT GGCTTCATTC AGCTCCGGTT CCCAACGATC AAGCGAGTT
ACATGATCCC
25  4081  CCAATGTTTG CAAAAAAGCG GTTAGCTCCT TCGTCTCTCC GATCGTTGTC
AGAAGTAGT
4141  TGGCCGCGAG GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCCTCT
ACTGTTCATGC
4201  CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCAATC
30  TGAGAATAGT
4261  GTATGCGGCG ACCGAGTTGC TCTTGCCCGG CGTCAATACG GGATAATACC
GCGCCACATA
4321  GCAGAACTTT AAAAGTGCTC ATCATTGGAA AACGTTCTTC GGGGCGAAAA
CTCTCAAGGA
35  4381  TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC
TGATCTTCAG
4441  CATCTTTTAC TTTCACCAGC GTTTCGGGT GAGCAAAAAA AGGAAGGCAG
AATGCCGCAA
4501  AAAAGGGAAT AAGGGCGACA CGGAATGTT GAATACTCAT ACTCTTCCTT
40  TTTCAATATT
4561  ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA CATATTGAA
TGTAATTAGA
4621  AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
GACGCTAAG
45  4681  AAACCATTAT TATCATGACA TTAACCTATA AAAATAGGCG TATCAGGAGG
CCCTTTCGTC

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The segment *rhaR* through *Prha* was taken from the *E. coli* chromosome using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with SalI followed by XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

SEQ ID NO.: 154

pMPX-71 arabinose-inducible expression vector

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1 TCGCGCGTTT CGTGATGAC GGTGAAACC TCTGACAT GCAGCTCCCG
GAGACGGTCA
61 CAGCTTGTCT GTAAGCGSAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG
TCAGCGGGTG
5 121 TTGGCGGGTG TCGGGGCTGG CTAACTATG CGGCATCAGA GCAGATTGTA
CTGAGAGTGC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC
ATCAGCGGCC
241 ATTCCGCATT CAGGCTGCGC AACTGTTGGG AAGGCGGATC GGTGCGGGCC
10 TCTTCGCTAT
301 TACGCCAGCT GCGGAAAGGG GGATGTGCTG CAAGCGGATT AAGTTGGGTA
ACGCCAGGGT

HindIII

15 361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAATGCCAA GCTTCAAGCC
GTCAATTGTC

Stop araC

20 421 TGATTCGTTA CCAATTATGA CAACTTGACG GCTACATCAT TCACTTTTTC
TTCACACCG
481 GCACGGAAT CGTCGGGCT GGCCCCGGTG CATTTTTTAA ATACCCGCGA
GAATAGAGT
541 TGATCGTCAA AACCAACATT GCGACCGACG GTGGCGATAG GCATCCGGGT
GGTGCTCAA
25 601 AGCAGCTTCG CTGGCTGAT ACGTTGCTCC TCGGCCACG TTAAGACGCT
AATCCCTAAC
661 TGCTGGCGGA AAAGATGTA CAGACGCGAC GGCACAAAG AACATGCTG
TGCACGCTG
721 GCGATATCAA AATTGCTGTC TGCCAGGTGA TCGCTGATGT ACTGACAAAG
30 CTCGCGTACC
781 CGATTATCCA TCGGTGGATG GAGCGACTCG TTAATCGCTT CCAATGCGCG
CAGTAACAAT
841 TGCTCAAGCA GATTATCGC CAGCAGCTCC GAATAGCGCC CTTCCCTTG
CCCGGCGTTA
35 901 ATGATTGTC CAAACAGTC GCTGAAATGC GGCTGCTGCG CTTTATCCGG
GCGAAAGAAC
961 CCCGTATTGG CAAATATTGA CCGCCAGTTA AGCCATTAT GCCAGTAGGC
GCGCGGACGA
1021 AAGTAAACCC ACTGGTGATA CCATTGCGCA GCCTCCGGAT GACGACCGTA
40 GTGATGAATC
1081 TCTCTGGCG GGAACAGCAA AATATCACCC GGTGCGGCAA CAAATTCTCG
TCCCTGATTT
1141 TTCACACCC CTTGACCGCG AATGTTGAGA TTGAGAATAT AACCTTTCAT
TCCAGCGGT
45 1201 CGTTCGATAA AAAAATCGAG ATAACCGTTG GCCTCAATCG GCGTTAAACC
GCGCACAGA
1261 TGGGCATTAA ACGAGTATCC CGGCAGCAGG GGATCATTTT GCGCTTCAGC
CATACTTTTC

Start araC

50 1321 ATACTCCGCG CATTCAGAGA AGAAACCAAT TGTCATATT GATCCAGACA
TGCCGTCAC

<--

55 1381 TGCGTCTTTT ACTGGCTCTT CTCGTAACC AAACCGGTAA CCCGCTTAT
TAAAGCATTT
1441 CTGTAACAAA GCGGACCAA AGCCATGACA AAAACGCGTA ACAAAAGTGT
CTATAATCAC
1501 GGCAGAAAAA TCCACATTGA TTATTGTCAC GCGTCACAC TTTGCTATGC
60 CATAGCATTT

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1561 TTATCCATAA GATTAGCGGA TCC'TACCTGA CGCTTTT'TAT CGCAACTCTC
TACTGT'TTCT

5 1621 CCATACCCGT TTTTTTGGGC TAGCAGGAGG SD PstI SalI XbaI CCCTGCAGGT CGACTCTAGA
GGATCCCCGC

1681 Stem-loop GCCCTCATCC GAAAGGGCGT KpnI ATTGGTACCG AGCTCGAATT CGTAATCATG
10 GTCATAGCTG

1741 TTTCTGTGT GAAATTGTTA TCCGCTCACA ATTCACACA ACATACGAGC
CGGAAGCATA
1801 AAGTGTAAG CCTGGGTGC CTAATGAGTG AGCTAACTCA CATTAATTGC
15 GTTCCGCTCA
1861 CTGCCCGCTT TCCAGTCGGG AAACCTGTGC TGCCAGCTGC ATTAATGAAT
CGGCCAACGC
1921 GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC
TGACTCGCTG
1981 CGCTCGGTGC TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGCGCGT
20 AATACGGTTA
2041 TCCACAGAAT CAGGGGATAA GCGAGGAAG AACATGTGAG CAAAGGCCA
GCAAAAGGCC
2101 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCC
25 CCCTGACGAG
2161 CATCAGAAA ATCGACGCTC AAGTCAGAGG TGGCGAAAC CGACAGGACT
ATRAAGATAC
2221 CAGGCGTTTC CCCCTGGAAG CTCCTCTGNG CGCTCTCCTG TTCCGACCCCT
GCCGCTTACC
2281 GGATACCTGT CCGCCTTCTC CCCTTCGGGA AGCGTGGCGC TTTCTCATAG
30 CTCACGCTGT
2341 AGGTATCTCA GTTCGGTGTG GGTGTTGCG TCCAAGCTGG GCTGTGTGCA
CGAACCCCCC
2401 GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA
35 CCCGTAAGA
2461 CACGACTTAT GCGCACTGCG AGCAGCCACT GGTAAACAGGA TTAGCAGAGC
GAGGTATGTA
2521 GGCGTGCTA CAGAGTTCCTT GAAGTGGTGG CCTAACTACG GCTACACTAG
AAGGACAGTA
2581 TTTGGTATCT GCGCTCTGCT GAAGCCAGIT ACCTTCGGAA AAAGAGTTGG
40 TAGCTCTTGA
2641 TCCGGCAAAC AAACCACGCG TGGTAGCGGT GGT'TTTTTTG TTTGCAAGCA
GCAGATTACG
2701 GCGAGAAAAA AAGGATCTCA AGAAGATCTC TTGATCTTTT CTACGGGGTC
45 TGACGCTCAG
2761 TGGAAAGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAG
GATCTTACC
2821 TAGATCCTTT TAAATTAAAA ATGAAGTTT TAAATCAATCT AAAGTATATA
TGAGTAAACT
50 2881 TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
CTGTCTATIT
2941 CGTTATCCA TAGTTGCCGT ACTCCCCGTC GTGTAGATAA CTACGATACG
GGAGGGCTTA
3001 CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
55 TCCAGATTTA
3061 TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGTCTCTGC
AACTTTATCC
3121 GCCTCCATCC AGTCTATTAA TTGTGCCGG GAAGCTAGAG TAAGTAGITC
GCCAGTAAAT

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The segment araC through Para was taken from pBAD24 using PCR added HindIII and modified aligned Shine-Delgarno (SD) sequence with PstI followed by SalI, XbaI, a stem-loop transcriptional stop sequence, and KpnI. The PCR product was cloned into pUC18 using HindIII and KpnI.

35 pMPX-68 melibiose-inducible expression vector

50 HindIII
361 TTTCCAGTC ACGACGTTGT AAAACGACGG CCAGTGCCA GCTTTTAGCC
GGGAAACGTC

55 421 TGGCGGCGCT GTTGGCTAAG TTTGCGGTAT TGTTCGGCGC ACATGCCGAC
ATATTTGCCG
481 AACGTGCTGT AAAAACGACT ACTTGAACGA AAGCCTGCCG TCAGGGCAAT
ATCGAGAATA

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541 CTTTATATCGG TATCGCTCAG TAACGCGCGA ACGTGGTTGA TCGCATCGC
GGTAATGTAC
601 TGTITTCATCG TCAATTGCAT GACCCGCTGG AATATCCCCA TTGCATAGTT
GGCGTTAAGT
5 661 TTGACGTGCT CAGCCACATC GTTGTATGGTC AGCGCTTGAT CATAGTTTTC
GGCAATAAAG
721 CCCAGCATCT GGCTAACATA AAATTGCGCA TGGCGCGAGA CGCTGTTTTT
GTGTGTGCGC
781 GAGGTITTTAT TGACCAGAAT CGGTTCCAG CCAGAGAGGC TAAATCGCTT
10 GAGCATCAGG
841 CCAATTTTAT CAATGGCGAG CTGGCGAATT TGCTCGTTGC GACTGTTTAA
TTCTCTCTGC
901 CAGCGCGCGA CTTCAAACGG GCTAAGTTGC TGTGTGCCA GTGATTTGAT
CACCATTGCC
15 961 TGAGTGACGT GGTAAATCAG GTCTTTATCC AGCGGCCAGG AGAGAAACAG
ATGCATCGGC
1021 AGATTAAAAA TCGCCATGCT GTGACAGGTT CCGGTATCTG TTAGTTGGTG
CGGTGTACAG
1081 GCCCAGAAC ACGTGATATG ACCCTGATTG ATATTCACTT TTTCATTGTT
20 GATCAGGTAT
1141 TCCACATCGC CATCGAAAGG CACATTCAT TCGACCTGAC CATGCCAGTG
GCTGTGCGGC
1201 ATGATATGCG GTGCGCGAAA CTCAATCTCC ATCCGCTGGT ATTCCGAATA
CAGCGACAGC
25
1261 GGGCTGCGGG TCTGTTTTTC GTCGTGCTG CACATAAACG TATCTGTATT
CATGGATGGC +1 MelR
30
1321 TCTCTTTTCT GGAATATCAG AATTATGCCA GGAGTGAGG AGGATGACTG
CGAGTGGGAG
1381 CACGTTTTTC ACCCTCTTCC CAGAGGGGCG AGGGAGCTCT CCGAGTATCA
TGAGGCCGAA
35 1441 AACTCTGCTT TTCAGGTAAT TTATTCCCAT AAATCAGAT TTAATGCTGC
TTCAGCGAGG
1501 ATCTGAGTTT ATGGGAATGC TCAACCTGGA AGCCGAGGTT TTTCTGCAGA
TTCCGCTGCC
40
SD SalI XbaI
1561 ATGATGAAGT TATTCAGCA AGCCAGGAGG TCGTCGACTC TAGAGGATCC
CGCGCCCTC
45
Stem-loop KpnI
1621 ATCCGAAAGG GCGTATTGGT ACCGAGCTCG AATTCGTAAT CATGGTCATA
GCTGTTTCTT
50
1681 GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG
CATAAAGTGT
1741 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGGC
CTCACTGCCC
1801 GCTTTCCAGT CGGGAACCT GTCTGCCAG CTGCATTAAT GAATCGGCCA
ACGCGCGGGG
55 1861 AGAGGCGGTT TGCGTATTGG GCGCTCTTCC GCTTCTCGC TCACTGACTC
GCTGCGCTCG
1921 GTCTTTCGGC TCGCGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
GTTATCCACA
1981 GAATCAGGGG ATAACGCAGG AAGAACAATG TGAGCAAAG GCCAGCAAAA
60 GGCCAGGAAC

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2041 CGTAAAAAGG CCGCGTTGCT GCGCTTTTTC CATAGGCTCC GCCCCCCCTGA
CGAGCATCAC
2101 AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG
ATACCAGGCG
5 2161 TTTC CCCCTG GAAGCTCCCT CGTGCGCTCT CCGTTCCGA CCCTGCCGCT
TACCGGATAC
2221 CTGTGCGCCT TTCTCCCTTC GGGGAAGCGTG GCGCTTTTCTC ATAGCTCAGC
CTGTAGGTAT
10 2281 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
CCCCGTTCAG
2341 CCGACCCGCT GCGCCTTATC CCGTAACTAT CGTCTTGAGT CCAACCCGGT
AAGACACGAC
2401 TTATCGCCAC TGCGAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA
TGTAGGCGGT
15 2461 GCTACAGAGT TCTTGAAGTG GTGGCTTAAC TACGGCTACA CTAGAAGGAC
AGTATTTGGT
2521 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
TTGATCCGGC
2581 AAACAACCA CCGCTGGTAG CGGTGGTTTIT TTTGTTTGCA AGCAGCAGAT
TACGCGCAGA
20 2641 AAAAAAGGAT CTCAAGAAGA TCCTTTTGATC TTTTCTACGG GGTCTGACGC
TCACTGGAAC
2701 GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA AAAGGATCTT
CACCTAGATC
25 2761 CTTTTAAAIT AAAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
AACTTGGTCT
2821 GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT
ATTTCTGTCA
2881 TCCATAGTTG CCTGACTCCC CGTGTGTAG ATAACTACGA TACGGGAGGG
CTTACCATCT
30 2941 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA
TTTATCAGCA
3001 ATAAACCAGC CAGCCGGAAG GGCGAGCGC AGAAGTGGT CTGCAACTTT
ATCCGCTTCC
35 3061 ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAAGTA GTTCGCCAGT
TAATAGTTTG
3121 CGCAACGTTG TTGCCATTGC TACAGGCATC GTGGTGTAC GCTCGTCGTT
TGGTATGGCT
40 3181 TCATTAGCT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
GTTGTGCAAA
3241 AAAGCGGTTA GTCCTTCGG TCCTCCGATC GTTGTCAAG GTAAGTTGGC
CGCAGTGTTA
3301 TCATCTATGG TTATGGCAGC ACTGCATAAT TCTTCTACTG TCATGCCATC
CGTAAGATGC
45 3361 TTTTCTGTGA CTGGTGAGTA CTCAACCAG TCATTCTGAG AATAGTGTAT
GCGGCGACCG
3421 AGTTGCTCTT GCCCGCGCTC AATACGGGAT AATACCGCG CACATAGCAG
AACTTTAAAA
3481 GTGCTCATCA TTGGA AAAACG TTCTTCGGGG CGAAARCTCT CAAGGATCTT
ACCGCTGTTG
50 3541 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC
TTTACTTTTC
3601 ACCACGCTTT CTGGGTGAGC AAAAACAGGA AGCAAAATG CCGCAAAAAA
GGGAAATAGG
55 3661 GCGACACGGA AATGTTGAAT ACTCATACTC TTCTTTTTC AATATTTATG
AAGCATTTAT
3721 CAGGGTTATG GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
TAAACAAATA
3781 GGGGTTCCCG GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC
CATTAITATC
60

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3841 ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC

SEQ ID NO.: 166

5

MalE (1-370) Factor Xa NTR (43-424) FLAG

SalI +1 MalE (1-370)
1 GTCGACATGAAAAATAAAACAGGTGCACGCATCCTCGCATTATCGGCATTAAACGACGATGATGTTT
10 1 M K I K T G A R I L A L S A L T T M M F
61 TCCGCTCTCGCTCTCGCCAAAAATCGAAGAGGTAAACTGGTAATCTGGATTAAACGCGCAT
21 S A S A L A K I E E G K L V I W I N G D
15 121 AAAGGCTATACCGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTA
41 K G Y N G L A E V G K K F E K D T G I K
181 GTCACCGTGTAGCATCCGGATAAACTGGAAGAGAAATCCCACAGGTTGCGGCAACTGGC
61 V T V E H P D K L E E K F P Q V A A T G
20 241 GATGGCCCTGACATTATCTTCTGGGACACGACCGCTTTGTGGCTACGCTCAATCTGGC
81 D G P D I I F W A H D R F G G Y A Q S G
301 CTGTGGCTGAAATCACCCGGACAAAGCGTTCCAGGACAAAGCTGTATCCGTTTACCTGG
25 101 L L A E I T P D K A F Q D K L T V P F T W
361 GATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGCTTATCG
121 D A V R Y N G K L I A Y P I A V E A L S
30 421 CTGATTTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCG
141 L I Y N K D L L P N P P K T W E E I P A
481 CTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCG
161 L D K E L K A K G K S A L M F N L Q E P
35 541 TACTTCACCTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGC
181 Y F T W P L I A A D G G Y A F K Y E N G
601 AAGTACGACATTAAAGACGTGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTC
40 201 K Y D I K D V G V D N A G A K A G L T F
661 CTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAA
221 L V D L I K N K H M N A D T D Y S I A E
45 721 GCTGCTTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGCGCATGGTCCAAC
241 A A F N K G E T A M T I N G P W A W S N
781 ATCGACACCGCAAGTGAATTATGGTGAACGGTACTGCGGACCTTCAAGGGTCAACCA
261 I D T S K V N Y G V T V L P T F K G Q P
50 841 TCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAAACGCGCCAGTCCGAACAAAGAG
281 S K P F V G V L S A G I N A A S P N K E
901 CTGGCGAAGAGGTTCTCGAAAACATCTGCTGACTGATGAAGGCTGGAAGCGGTTAAT
55 301 L A K E F L E N Y L L T D E G L E A V N
961 AAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGAT
321 K D K P L G A V A L K S Y E E E L A K D

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1021 CCACGTATTGCCGCCACCATGGAAAACGCCAGAAAGGTGAATCATGCCGAACATCCCG
341 P R I A A T M E N A Q K G E I M P N I P

Factor Xa +43 NTR

5 1081 CAGATGTCGCTTTCTGGTATGCCGTGCTGATCGAAGGCCGCACCTCGGAATCCGACAG
361 Q M S A F W Y A V L I E A R T S E S D T

1141 GCAGGCCCAACAGCGACCTGGACGTGAACACTGACMTTATTCGAAGGTGCTGGTGACT
381 A G P N S D L D V N T D I Y S K V L V T

10 1201 GCTATATACCTGGCACTCTTCGTGGTGGGCACTGTGGGCAACTCCGTGACAGCCTTCACT
401 A I Y L A L F V V G T V G N S V T A F T

1261 CTAGCGCGGAAGAAGTCACTGCAGAGCCTGCAGAGCACTGTGCATTACCACTGGGAGC
421 L A R K K S L Q S L Q S T V H Y H L G S

15 1321 CTGGCACTGTGCGACCTGCTTATCTCTTCTGCTGGCCATGCCCGTGAGCTATACAACCTC
441 L A L S D L L I L L A M P V E L Y N F

20 1381 ATCTGGGTACACCATCCCTGGGCCCTTGGGGAGCGCTGGCTGGCGTCACTATTTCCTG
461 I W V H H P W A F G D A G C R G Y Y F L

1441 CGTGATGCTGCACCTATGCCACAGCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTAC
481 R D A C T Y A T A L N V A S L S V E R Y

25 1501 TTGGCACTGTGCCATCCCTTCAAGCCCAAGACCTCATGTCCCGCAGCGCACCAAGAAA
501 L A I C H P F K A K T L M S R S R T K K

1561 TTCATCAGTGCCATATGGCTAGCTTGGCGCTGTGGCTATACCCATGCTTTTACCATTG
521 F I S A I W L A S A L L A I P M L F T M

30 1621 GGCCTGCAGAACCGCAGTGGTACGGCAGCACCCCTGGCGGCCTGTGTGTGCACACCCATT
541 G L Q N R S G D G T H P G G L V D C T P I

35 1681 GTGGACACAGCCACTGTCAAGGTGCTCATCCAGGTTAACACCTTCATGTCTTCTGTIT
561 V D T A T V K V V I Q V N T F M S F L F

1741 CCCATGTTGGTCACTCTCCATCCTAAACACCGTGATTGCCAACAACTGCACGTATGSGT
581 P M L V I S I L N T V I A N K L T V M V

40 1801 CACCAGCCGCCGAGCAGGGCCAGTGTGCACCGTGGGCACACAAACGTTTATAGCAC
601 H Q A A E Q G R V C T V G T H N G L E H

1861 AGCACGTTCAACATGACCATCGAGCCGGTGTGTCCAGGCCCTGCGCCACGGAGTCTCTC
621 S T F N M T I E P G R V Q A L R H G V L

45 1921 GTCTTACGTGCTGTGTCATTCCTTTTGGTCTGTGGTCTGCCCTACCACTGCGACGC
641 V L R A V V I A F V V C W L P Y H V R R

50 1981 CTGATGTTCTGCTATATCTCGGATGAACAGTGGACTACGTTCTCTTGTGATTTCTACCA
661 L M F C Y I S D R Q W T T F L F D Y H

2041 TATTTCTACATGCTAACCAACGCTCTCTTCTACGTACGCTCCGCCATCAATCCCATCTC
681 Y F Y M L T N A L F Y V S S A I N P I L

55 2101 TACAACCGTCTCCGCCAACTTCCGCCAGGTCTTTCGTCCAGCTGGCGTGCCTTTGT
701 Y N L V S A N F R Q V F L S T L A C L C

2161 PCTGGTGGCGCCACCGCGAAGAAGAGGCCAACGTTCTCCAGAGGCCAACACGATG
721 P G W R H R R K K R P T F S R K P N S M

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SEQ ID NO.: 169

30 MaleE (1-370) Factor Xa NTR (43-424) TrxA (2-109) FLAG

231/268

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541 TACTTTCACCTGGCGCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAGTAGTGA AAAACGGC
181 Y F T T W P L I A A D G G Y A F K Y E N G

5 601 AAGTACGACATTA AAGACGTGGGCGTGGATAACGCTGGCGGAAAGCGGGTCTGACCTTC
201 K Y D I K D V G V D N A G A K A G L T F

661 CTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAA
221 L V D L L I K N K H M N A D T D Y S I A E

10 721 GCTGCCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGGCGATGCTCCAAC
241 A A F N K G E T A M T I N G P W A K S N

781 ATCGACACCAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCA
261 I D T S K V N Y G V T V L P T F K G Q P

15 841 TCCAAACCGTTTCGTTGGCGTGTGAGCGCAGGTATTACGCCCGCGAGTCCGAACAAAGAG
281 S K P F V G V L S A G I N A A S P N K E

901 CTGGCGAAAGAGTTCTCTGAAAATATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAAT
301 L A K E F L E N Y L L T D E G L E A V N

961 AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGAT
321 K D K P L G A V A L K S Y E E E L A K D

25 1021 CCACGTATTGCCGCCACCATCGAAAACGCCAGAAAGGTGAATCATGCCGAACATCCCG
341 P R I A A T M E N A Q K G E I M P N I P

Factor Xa +43 NTR
1081 CAGATGTCGCTTTCTGATGCGGTGCTGATCGAAGCCCGCACTTCGGAATCCGACAGC
361 Q M S A F W Y A V L I E A R T S E S D T

1141 GCAGGCCCAACAGCGACCTGGACGTGAACACTGACATTTATTCAGAGGTGCTGGTGACT
381 A G P N S D L D V N T D I Y S K V L V T

35 1201 GCTATATACCTGGCACTCTTCGTGGTGGGCACTGTGGGCACTCCGTGACAGCCTTCACT
401 A I Y L A L F V V G T V G N S V T A F T

1261 CTAGCGCGGAAGAGTCACTGCAGAGCCTGCAGAGCACTGTGCAATTACCACTGGGCAGC
421 L A R K K S L Q S L Q S T V H Y H L G S

40 1321 CTGGCACTGTGGGACCTGCTTATCCTTCTGCTGGCCATGCCCGTGGAGCTATACAACTTC
441 L A L S D L L I L L A M P V E L Y N F

1381 ATCTGGGTACACCATCCCTGGGCTTTGGGGACGCTGGCTGCGGTGGCTACTATTTCTCTG
461 I W V H H P W A F G D A G C R G Y Y F L

1441 CGTGATGCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGAGCGCTAC
481 R D A C T Y A T A L N V A S L S V E R Y

50 1501 TTGGCCATTCGCATCCCTTCAAGGCCAAGACCCCTCATGTCCCGCAGCGCACCACGAAGA
501 L A I C H P F K A K T L M S R S R T K K

1561 TTCATCAGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCCATGCTTTTACCATTG
521 F I S A I W L A S A L L A I P M L F T M

55 1621 GGCCTGCAGAACCGCAGTGGTACGGCAGCACCCCTGGCGGCTGGTGTGCACACCCATT
541 G L Q N R S G D G T H P G G L L V C T P I

1681 GTGGACACAGCCACTGTCAAGGTGCTCATCCAGGTAAACCACTTCATGTCTCTCTGTTT
561 V D T A T V K V V I Q V N T F M S F L F

60

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SEO ID NO.: 170

233/268

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SalI +1 Male leader (1-28)
1 gtcgcacATGAAAAATAAAACAGGTGCAGCATCCTCGCATATATCCGCATTAAACAGCATGATGTTT
1 M K I K T G A R I L A L S A L T T M M F

5 Factor Xa +43 NTR
61 TCCGCCTCGGCTCTCGCCAAAATCATCGAAGCCCGCAGCTCGGAATCCGACACGGCAGGG
21 S A S A L A K I I E A R T S E S D T A G

10 121 CCCAACACGACCTGGACGTGAACACTGACATTTATTCGAAGGTGCTGGTGACTGCTATA
41 P N S D L D V N T D I Y S K V L V T A I

15 181 TACCTGGCACTCTTCGTGGTGGGCACCTGTGGCAACTCCGTGACAGCCTTCACTCTAGCG
61 Y L A L F V V G T C T V G N S V T A F T L A

20 241 CGGAAGTCACTGCAGAGCCCTGCAGAGCACTGTGCAATTACCACTTGGCAGCCTGGCA
81 R K K S L Q S L Q S T V H Y H L G S L A

25 301 CTGTGGACCTGCTTATCTCTGTGTCGCCATGCCCGTGGAGCTATACAACCTTCATCTGG
101 L S D L L I L L L A M P V E L Y N F I W

30 361 GTACACCATCCCTGGGCCCTTTGGGGACGCTGGCTGCCGTGGCTACTATTTCTCGCGTG
121 V H H P W A F G D A G C R G Y Y F L R D

35 421 GCCTGCACCTATGCCACAGCCCTCAATGTAGCCAGCCTGAGTGTGGAGCGCTACTTGGCC
141 A C T Y A T A L N V A S L S V E R Y L A

40 481 ATCTGCCATCCCTTCAAGGCCAAGACCCCTCATGTCCCGCAGCCGACCAAGAAATTCATC
161 I C H P F K A K T L M S R S R T K K F I

45 541 AGTGCCATATGGCTAGCTTCGGCGCTGCTGGCTATACCACTGCTTTTCACCATGGCGCTG
181 S A I W L A S A L L A I P M L F T M G L

50 601 CAGAACCGCAGTGGTGACGGCAGCACCCCTGGCGGCTGGTGTGACACCCATTGTGGAC
201 Q N R S G D G T H P G G L V C T P I V D

55 661 ACAGCCACTGTCAAGTCTGTATCCAGGTTAAACACCTTCATGTCTCTCTGTTTCCCATG
221 T A T V K V V I Q V N T F M S F L F P M

60 721 TTGGTCATCTCCATCTAAACACCGTGATGGCAACAACTGACAGTCATGTGTCACACG
241 L V I S I L N T V I A N K L G A T V M V H I

65 781 GCCCGCAGCAGGGCCGAGTGTGCACCGTGGGCACACACAAGCTTTAGAGCACAGCAGC
261 A A E Q G R V C T V G T H N G L E H S T

70 841 TTCAACATGACCATCGAGCCGGGTGTTGTCAGGCCCTGCGCCACGGAGTCCTGTTCTTA
281 F N M T I E P G R V Q A L R H G V L V L

75 901 CGTGCTGTGTCATTGCGCTTTGTGGTGTGCTGGCTGCCCTACCACTGCGCACGCTGATG
301 R A V V I A F V V C W L P Y H V R R L M

80 961 TTTCTGTATATCTCGGATGAACAGTGGACTACGTTCTCTCTCGATTCTACCACTATTTC
321 F C Y I S D E Q W T T F L F D F Y H Y F

85 1021 TACATGCTAACCAACGCTCTCTTCTACGTACGTCGCCCATCAATCCATCTCTTCAAC
341 Y M L T N A L F Y V S S A I N P I L Y N

90 1081 CTGGTCTCCGCCAACTCCGCCAGGTCCTTCTGTCCACGCTGGCCTGCCCTTGTCTGGG
361 L V T S A N F R Q V F L S T L A C L C P G

95 1141 TGGCGCCACCGCCGAAAGAAGAGGCCAACGTTCTCCAGGAAGCCCAACGATGTCCAGC

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381 W R H R R K K R P T F S R K P N S M S S
NotI +2 TrxA
1201 AACCATGCGCTTTTCCACCAGCGCCACCGGGAGACCCCTGTACgagggcgcaAGCGATAAA
5 401 N H A F S T S A T R E T L Y A A A S D K
1261 ATTATTACCTGACTGACGACAGTTTTGGACACGGATGTACTCAAAGCGGACGGGGGATC
421 I I H L T D D S F D T D V L K A D G A I
10 1321 CTCGTCGATTTCCTGGGCGAGTGGTGCCTGCGTCCGTGCAAAATGATGCCCCGATTCTGGAT
441 L V D F W A E W C G P C K M I A P I L D
1381 GAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAAC
461 E I A D E Y Q G K L T V A K L N I D Q N
15 1441 CCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTGCTGCTGTTCAAAAC
481 P G T A P K Y G I R G I P T L L L F K N
1501 GGTGAAGTGGCGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAGAGTTCCTC
20 501 G E V A A T K V G A L S K G Q L K E F L
NotI Flag stop KpnI
1561 GACGCTAACCTGGCagggcgcaGATTATAAGATGACGATGACAAATAAAGTTACC
521 D A N L A A A A D Y K D D D D K
25

SEQ ID NO.: 188

30 Human β 2AR GS1 α chimeric fusion

SalI +1 B2AR
1 GTCGACATGG GGCAACCCGG GAACGGCAGC GCCTCTCTGC TGGCACCCAA
TGGAAGCCAT
35 61 GCGCCGGACC ACGACGTCAC GCAGCAAAGG GACGAGGTGT GGGTGGTGGG
CATGGGTCATC
121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTTGGCAATG TGCTGGTCAT
CACAGCCATT
40 181 GCCAAGTTGG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT
241 GATCTGGTCA TGGGCCTAGC AGTGGTGCC TTTGGGGCG CCCATATTCT
TATGAAAATG
301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
45 GTGCGTCAG
361 GCCAGCATTG AGACCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACT
421 TTCAAGTACC AGAGCTGTCT GACCAAGAA TAAAGCCGGG TGATCATTTCT
GATGGTGTG
50 481 ATTGTGTGAG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCCCTC TACGTTCCTC TGGTGATCAT
55 GGTCTTCGTC
661 TACTCCAGGG TCCTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GCGGACGGG
GCATGGACTC

WO 03/07214

PCT/US02/16877

781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
 AGGCATCATC
 841 ATGGGCACTT TCACCTCTG CTGGCTGCC TTCTTCATG TTAACATTGT
 GCATGTGATC
 5 901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCTCTCTAA ATTGGATAGG
 CTATGTCAAT
 961 TCTGGTTTCA ATCCCCITAT CTACTGCCG AGCCAGATT TCAGGATTGC
 CTTCCAGGAG
 1021 CTTCTGTGCC TGCAGGTC TTCTTTGAAG GCCTATGGCA ATGGCTACTC
 10 CAGCAACGGC
 1081 AACACAGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
 ACTGCTGTGT
 1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GCCATCAAG GTACTGTGCC
 TAGCGATAAC
 15
 Last B2AR Linker
 sequence
 1201 ATTGATTAC AAGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG
 20 TGGCCAGACE
 PstI XhoI +2 GS1 alpha
 1261 GTCACCAACC TGCAGCTCGA GGGCTGCCCT GGGACACAGTA AGACCGAGGA
 CCAGCGCAAC
 25
 1321 GAGGAGAAG CGCAGCGTGA GGCCAACAAA AGATCGAGA AGCAGCTGCA
 GAAGGACAAG
 1381 CAGGTCTACC GGGCCACGCA CCGCCTGCTG CTGCTGGGTG CTGGAGAATC
 TGGTAAAAGC
 30 1441 ACCATTGTGA AGCAGATGAG GATCCTGCAT GTTAATGGGT TTAATGGAGA
 CAGTGAGAAG
 1501 GCAACCAAAG TGCAGGACAT CAAAAACAAC CTGAAAGAGG CGATTGAAAC
 CATTGTGGCC
 1561 GCCATGAGCA ACCTGGTSCC CCCCCTGGAG CTGGCCAACC CCGAGAACCA
 GTTCAGAGTG
 35 1621 GACTACATCC TGAGTGTGAT GAACGTGCCCT GACTTTGACT TCCCTCCCGA
 ATTCATGAG
 1681 CATGCCAAGG CTCTGTGGGA GGATGAAGGA GTGCTGCCCT GCTACGAACG
 CTCACACGAG
 40 1741 TACCAGCTGA TTGACTGTGC CCAGTACTTC CTGGACAAGA TCGACGTGAT
 CAAGCAGGCT
 1801 GACTATGTGC CGAGCGATCA GGACCTGCTT CGCTCGCGTG TCCTGACTTC
 TGGAACTTTT
 1861 GAGACCAAGT TCCAGGTGGA CAAAGTCAAC TTCCACATGT TTGACGTGGG
 TGGCCAGCGC
 45 1921 GATGAACGCC GCAAGTGGAT CCAAGTCTTC AACGATGTGA CTGCCATCAT
 CTTCTGTGTG
 1981 GCCAGCAGCA GCTACAACAT GGTCTACCCG GAGGACAACC AGACCAACCG
 CCTGCAGGAG
 50 2041 GCTCTGAACC TCTTCAAGAG CATCTGGAAC AACAGATGGC TGCACCAAT
 CTCTGTGATC
 2101 CTGTTCTCTCA ACAAGCAAGA TCTGCTGCTG GAGAAAGTCC TTGCTGGGAA
 ATCGAAGATT
 2161 GAGGACTACT TTCCAGAATT TGCTGCTAC ACTACTCTCT AGGATGCTAC
 TCCGAGCCC
 55 2221 GGAGAGGACC CACGCGTGAC CCGGCCCAAG TACTTCAITC GAGATGATTC
 TCTGAGGATC
 2281 AGCACTGCCA GTGGAGATGG GCCTCACTAC TGCTACCCCT ATTTCACCTG
 CGCTGTGGAC

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2341 ACTGAGAACA TCCGCCGTGT GTTCAACGAC TGCCGTGACA TCATTACGG
CATGCACCTT

5 2401 CGTCAGTACG AGCTGCTCAT CGATTAAATAA TCTAGAGGAT CCCCGCGCCC
TCATCCGAAA

2461 GGGCG

10

SEQ ID NO.: 190

Human β 2AR stop GS1 α transcriptional fusion

15 PstI +1 B2AR
1 GTCCGACATGG GGCAACCCGG GAACGGCAGC GCCTTCTTGC TGGCACCCAA
TGAAGCCAT

20 61 GCGCCGGACC ACGACGTACG GCAGCAAAGG GACGAGGTGT GGTGTGTGG
CATGGGCATC
121 GTCATGTCTC TCATCGTCCT GGCCATCGTG TTGGCAATG TGCTGSTCAT
CACAGCCATT
25 181 GCCAAGTTCG AGCGTCTGCA GACGGTCACC AACTACTTCA TCACTTCACT
GGCCTGTGCT
241 GATCTGGTCA TGGGCCTAGC AGTGGTGCCC TTTGGGGCGG CCCATATTCT
TATGAAAATG
30 301 TGGACTTTTG GCAACTTCTG GTGCGAGTTT TGGACTTCCA TTGATGTGCT
GTGCGTCACG
361 GCCAGCATTG AGACCTGTG CGTGATCGCA GTGGATCGCT ACTTTGCCAT
TACTTCACCT
421 TTCAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGGG TGATCATTCT
GATGGGTGG
35 481 ATTGTGTACG GCCTTAYCTC CTTCTTGCCC ATTCAGATGC ACTGGTACAG
GGCCACCCAC
541 CAGGAAGCCA TCAACTGCTA TGCCAATGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCTCTT TACGTTCGCC TGGTGATCAT
GGTCTTCGTC
40 661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GCGGGACGGG
GCATGGACTC
45 781 CGCAGATCTT CCAAGTTCTG CTTGAAGGAG CACAAAGCCC TCAAGACGTT
AGGCATCATC
841 ATGGGGCACTT TCACCCCTCG CTGGCTGCCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAAOC TCATCCGTAA GGAAGTTTAC ATCTTCCTAA ATTGGATAGG
CTATGTCAAT
50 961 TCTGGTTTCA ATCCCTTAT CTACTGCCGG AGCCCGAGAT TCAGGATTGC
CTTCCAGGAG
1021 CTTCTGTGCC TGCGCAGGTC TTCTTTGAAG GCTATGGCA ATGGCTACTC
CAGCAACGGC
55 1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
1141 GAAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

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Last B2AR Linker

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sequence
1201  ATTGATTAC  AAGGGAGGAA  TTGTAGTACA  AATGACTCAC  TGCTAGAGCG
TGGCCAGACG
5
          PstI  Stop      SD      XhoI  +2 GS1 alpha
1261  GTCACCAACC  TGCAGTAATA  ATCAAGGAGG  CCCTCGAGAT  GGGCTGCCTC
GGGAACAGTA

10
1321  AGACCGAGGA  CCAGCGCAAC  GAGGAGAAGG  CGCAGCGTGA  GGCCACACAA
AAGATCGAGA
1381  AGCAGCTGCA  GAAGGACAAG  CAGGTCTACC  GGGCCACGCA  CCGCCTGCTG
CTGCTGGGTG
15
1441  CTGGAGAATC  TGGTAAAGC  ACCATTGTGA  AGCAGATGAG  GATCCTGCAT
GTTAARTGGT
1501  TTAATGGAGA  CAGTGAGAAG  GCAACCAAG  TGCAGGACAT  CAAAAACAAC
CTGAAAGAGG
20
1561  CGATTGAAAC  CATTGTGGCC  GCCATGAGCA  ACCTGGTGCC  CCCCCTGGAG
CTGGCCAACC
1621  CCGAGAACCA  GTTCAGAGTG  GACTACATCC  TGAAGTGTAT  GAACGTGCCT
GACTTTGACT
1681  TCCCTCCCGA  ATTCTATGAG  CATGCCAAGG  CTCTGTGGGA  GGATGAAGGA
GTGGGTGCCT
25
1741  GCTACGAACG  CTCCAACGAG  TACCAGCTGA  TTGACTGTGC  CAGTACTTTC
CTGGACAAGA
1801  TCGACGTGAT  CAAGCAGGCT  GACTATGTGC  CGAGCGATCA  GGACCTGCTT
CGCTGCCGTG
1861  TCCTGACTTC  TGGAACTTTT  GAGACCAAGT  TCCAGGTGGA  CAAAGTCAAC
TTCCACATGT
30
1921  TTGACGTGGG  TGGCCAGCGC  GATGAACGCC  GCAAGTGGAT  CCAAGTCTTC
AACGATGTGA
1981  CTGCCATCAT  CTTCTGTGTG  GCCAGCAGCA  GCTACAACAT  GGTCACTCCG
GAGGACAACC
35
2041  AGACCAACCG  CCTGCAGGAG  GCTCTGAACC  TCTTCAAGAG  CATCTGGAAC
AACAGATGGC
2101  TGGCACCATT  CTCTGTGATC  CTGTTCTTCA  ACAAGCAAGA  TCTGCTCGCT
GAGAAAGTCC
2161  TTGCTGGGAA  ATCGAAGATT  GAGGACTACT  TTCCAGAAAT  TGCTCGCTAC
ACTACTCCTG
40
2221  AGGATGCTAC  TCCCAGAGCC  GGAGAGGACC  CACGCGTGAC  CCGGGCCAAG
TACTTCATT
2281  GAGATGAGTT  TCTGAGGATC  AGCACTGCCA  GTGGAGATGG  CGGTCACTAC
TGCTACCCCTC
45
2341  ATTTCACTCT  CGCTGTGGAC  ACTGAGAACA  TCCGCCGTGT  GTTCAACGAC
TGCCGTGACA

                                ClaI  Stop      XbaI
50
2401  TCATTTCAGC  CATGCACCTT  CGTCAGTACG  AGCTGCTCAT  CGATTATATA
TCTAGAGGAT

          Stem-loop
2461  CCCCCGCCCC  TCATCCGAAA  GGCGC

```

55

SEQ ID NO.: 192

Human GS1α

WO 03/072014

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XhoI

1
CTCGAGATGGGCTGCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT

5 1 M G C L G N S K T E D Q R N E E K A Q R

61 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG

21 E A N K K I E K Q L Q K D K Q V Y R A T

10 CACCGCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAGCACCATTGTGAAGCAGATG

41 H R L L L L G A G E S G K T I V K Q M

181 AGGATCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACCAAGTGCAAGGAC

61 R I L H V N G F N G D S E K A T K V Q D

15 241 ATCAAAAACCAACCTGAAAGAGGCGATTGAACCATTTGTGGCCGCCATGAGCAACCTGGTG

81 I K N N L K E A I E T I V A A M S N L V

301 CCCCCGTGGAGCTGGCCAACCCCGAGAACCAGTTTCAGAGTGAGTACTACATCCTGAGTGTG

101 P P V E L A N P E N Q F R V D Y I L S V

361 ATGAACGTCCTGACTTTGACTTCCCTCCCGAATTTCTATGAGCATGCCAAGGCTCTGTGG

121 M N V P D F D F P P P E F Y E H A K A L W

25 421 GAGGATGAAGAGTGCCTGCTGCTACGAACGCTCCAACGAGTACCAGTGTATGACTGT

141 E D E G V R A C Y E R S N E Y Q L I D C

481 GCCCAGTACTTCCCTGGACAAGATCGAGCTGATCAAGCAGGCTGACTATTGTGCCGAGCGAT

161 A Q Y F L D K I D V I K Q A D Y V P S D

30 541 CAGGACCTGCTTCGCTGCCGTGTCTGACTTCTGGAATCTTTGAGACCAAGTTCAGAGTG

181 Q D L L R C R V L T S G I F E T K F Q V

601 GACAAAGTCAACTCCACATGTTTGACGTGGGTGCCAGCGGATGAACGCCCAAGTGG

35 201 D K V N F H M F D V G G Q R D E R R K W

661 ATCCAGTGTCTTCAACGATGTGACTGCCATCATCTTCGTGTGGCCAGCAGCAGCTACAAC

221 I Q C F N D V T A I I F V V A S S S Y N

40 721 ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAG

241 M V I R E D N Q T N R L Q E A L N L F K

781 AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATCCTGTTCCTCAACAAGCAA

261 S I W N N R W L R T I S V I L F L N K Q

45 841 GATCTGCTCGCTGAGAAAGTCCTTGTGGGAAATGAAGATTGAGGACTACTTTCCAGAA

281 D L L A E K V L A G K S K I E D Y F P E

901 TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTG

50 301 F A R Y T T P E D A T P E P G E D P R V

961 ACCCGGGCAAGTACTTTCATTCGAGATGAGTTTCTGAGGATCAGCATCTGCCAGTGAGAT

321 T R A K Y F I R D E F L R I S T A S G D

55 1021 GGGCGTCACTACTGCTACCTCATTTACCTGCGCTGTGGACACTGAGAACATCCGCGT

341 G R H Y C Y P H F T C A V D T E N I R R

1081 GTGTTCAAGACTGCCGTGACATCATTCAGCGCATGCACCTTCGTCACTACGAGTCTCTC

361 V F N D C R D I I Q R M H L R Q Y E L L

60

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240/268

PCT/US02/16877

Clai

15

KhoI

WO 03/072014

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841 GAGAAAATCATGTATTCCCATCTAGTCGACTACTTCCCAGAAATATGATGGACCCAGAGA
281 E K I M Y S H L V D Y F P E Y D G P Q R

5 901 GATGCCCGGCGAGCCCGAGAAATTCATTCTGAAGATGTTCCGTGGACCTGAACCCAGACAGT
301 D A Q A A R E F I L K M F V D L N P D S

961 GACAAAATTATCTACTCCCACTTCACTGCGCCACAGACACCGAGAATATCGCTTTGTC
321 D K I I Y S H F T C A T D T E N I R F V

10

ClaI
1021
TTTGTGCGCGTCAAGGACACCATCTCTCCAGTTGAACCTGAAGGAGTACAATCTGGTCATCGAT

15 341 F A A V K D T I L Q L N L K E Y N L V

SEQ ID NO.: 195

20 Human Glc

XhoI

1 CTCGAGATGGGCTGCACCGTGAAGCGCGAGGACAAGCGCGCGCGAGCGCTCTAAGATGATCGAC
25 1 M G C T V S A E D K A A A E R S K M I D

61 AAGAACCTCGGGAGGACGGAGAGAAGCGCGCGCGGAGGTGAAGTTGCTGCTGTTGGGT
21 K N L R E D G E K A A R E V K L L L L G

30 121 GCTGGGAGTCAAGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCAAGAGGATGGC
41 A G E S G K S T I V K Q M K I I H E D G

181 TACTCCGAGGAGGAATGCCGCGCAGTACCGGGCGGTTGTCTACAGCAACACCATCCAGTCC
61 Y S E E E C R Q Y R A V V Y S N T I Q S

35 241 ATCATGGCCATTGTCAAAGCCATGGGAAACCTGCAGATCGACTTTGGCGACCCCTCCAGA
81 I M A I V K A M G N L Q I D F A D P S R

301 GCGGACGACGCCAGGCAGCTATTGCACTGTCTCTGACCCGCGAGGAGCAAGGCGTGCTC
40 101 A D D A R Q L F A L S C T A E E Q G V L

361 CCTGATGACCTGTCCGGCGTCTATCCGAGGGCTCTGGGCTGACCATGTGTGACAGGCGTGC
121 P D D L S G V I R R L W A D H G V Q A C

45 421 TTGGCGGCTCAAGGGAATACCAGCTCAACGACTCAGTGCCTACTACCTGAACGACCTG
141 F G R S R E Y Q L N D S A A Y Y L N D L

481 GAGCGTATTGCACAGAGTGACTACATCCCCACACAGCAAGATGTGTACGGACCCCGTA
161 E R I A Q S D Y I P T Q Q D V L R T R V

50 541 AAGACCACGGGATCGTGGAGACACACTTCACCTTCAAGGACCTACACTTCAAGATGTTT
181 K T T G I V E T H F T F K D L H F K M F

601 GATGTGGGTGGTCAGCGTCTGAGCGGAAGAAGTGGATCCACTGCTTTGAGGCGCTCACA
55 201 D V G G Q R S E R K K W I H C F E G V T

661 GCCATCATCTTCTGCGTAGCCCTTGAGCGCCTATGACTTGGTGTAGCTGAGGACGAGGAG
221 A I I F C V A L S A Y D L V L A E D E E

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721 ATGAACCGCATGTCATGAGAGCATGAAGCTATTTCGATAGCATCTGCAACAACAAGTGGTTC
241 M N R M H E S M K L F D S I C N N K W F
5 781 ACAGACACGTCCTCATCTCTTCTTCAACAAGAAGGACCTGTTTGAGGAGAAGATCACA
261 T D T S I I L F L N K K D L F E E K I T
841 CACAGTCCCTTGACCATCTGCTTCCCTGAGTACACAGGGGCCAACAAATATGATGAGGCA
281 H S P L T I C F P E Y T G A N K Y D E A
10 901 GCCAGCTACATCCAGAGTAAGTTTGAGGACCTGAATAAGCGCAAGACCAAGGAGATC
301 C A S Y I Q S K F E D L N K R K D T K E I
961 TACACGCACTTCACGTGCGCCACCGACCAAGAAGCTGCGAGTTCGTGTTTGACCGCTC
321 Y T H F T C A T D T K N V Q F V F D A V
15
1021 ACCGATGTTCATCATCAAGAACAACCTGAAGGACTGCGGCCTCTTTCATGCAT
341 T D V I I K N N L K D C G L F

Clal

20

SEQ ID NO.: 196

Human Gα12/13

25

XhoI
1 CTCGAGATGTCCGGGGTGGTGCAGGACCTCAGCCGCTGCTGCTCGCGCGAGCGCGCGGGCC
1 M S G V V R T L S R C L L P A E A G G A
30 61 CGCGAGCGCAGGGCGGGCAGCGCGCGCGAGCGCGAGCGCGCGCGCGCGCGGAGGCGTATC
21 R E R R A G S G A R D A E R E A R R R S
121 CGCGACATCGACGCGCTGCTGGCCCGCAGCGCGCGCGCGCTCGCGCGCTGCTGAAGATC
41 R D I D A L L A R E R R A V R R L V K I
35 181 CTGCTGCTGGCGCGGGCGAGAGCGGCAAGTCCACGTTCTCAAGCAGATGCGCATCATC
61 L L L G A G E S G K S T F L K Q M R I I
241 CACGGCGCGAGTTTCGACCAGAAGCGCTGCTGGAGTTTCGCGACACCATCTTCGACAAC
40 81 H G R E F D Q K A L L E F R D T I F D N
301 ATCTCAAGGGCTCAAGGGTCTTGTGTGATGCACGAGATAAGCTTGGCATCTCTTGGCAG
101 I L K G S R V L V D A R D K L G I P W Q
45 361 TATTCTGAAATGAGAAGCATGGATGTTCTGATGGCCTTCGAGAACAGGCGGGGCTG
121 Y S E N E K H G M F L M A F E N K A G L
421 CCTGTGGAGCGCGCCACTTCCAGCTGTACGTCCCGGCCCTGAGCGCACTTCGAGGGAT
141 P V E P A T F Q L Y V P A L S A L W R D
50 481 TCTGGCATCAGGAGGCTTTCAGCCGGAGAAGCGAGTTTCAGCTGGGGAGTCCGTGAAG
161 S G I R E A F S R R S E F Q L G E S V K
541 TACTTCTGGACAACCTTGGACCGGATCGGCCAGCTGAATTACTTCTTAGTAAGCAAGAT
55 181 Y F L D N L D R I G Q L N Y F P S K Q D
601 ATCTGTGCTGGCTAGGAAAGCCACCAAGGAATTGTGAGCATGACTTCGTTATTAAAG
201 I L L A R K A T K G I V E H D F V I K K

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35

SEO ID NO.: 205

40 Human β 2AR-ToxR (5-141) chimera stop GS1 α -ToxR (5-141) chimera transcriptional fusion

45

	61	GCGCCGACC	ACGACGTCAC	GCACGAAAG	GACGAGGTGT	GGGTGTGTGG
		CATGGGCAT				
50	121	GTGTCGTCTC	TCATCGTCTC	GGCCATCGTG	TTTGGAATG	TGCTGTGTCAT
		CACAGGCATT				
	181	GCCAAAGTTC	AGCGCTGCGA	GACGGTCACC	AACTACTTCA	TCACCTTCACT
		GGCCTGTGCT				
	241	GATCTGGTCA	TGGGCTAGC	AGTGGTGCC	TTTGGGGCCG	CCCATATTCT
55		TATGAAAATG				
	301	TGGACTTTTG	GCAACTTCTG	GTGCGAGTTT	TGGACTTCCA	TGTATGTGCT
		GTGCGTCACG				
	361	GCCAGCATTG	AGACCTCTGT	CGTGATCGCA	GTGGATCGCT	ACTTTGCCAT
		TACTTCACT				

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421 TTCAAGTACC AGAGCCTGCT GACCAAGAAT AAGGCCCGG TGATCATCT
GATGGTGG
481 ATTGTGTGTCAG GCCTTAYCTC CTCTTGCCCT ATTGAGATGC ACTGGTACAG
GGCCACCCAC
5 541 CAGGAAGCCA TCAACTGCTA TGCCARTGAG ACCTGCTGTG ACTTCTTCAC
GAACCAAGCC
601 TATGCCATTG CCTCTTCCAT CGTGTCTCTC TACGTTCCCC TGGTGTATCAT
GGTCTTCGTC
661 TACTCCAGGG TCTTTCAGGA GGCCAAAAGG CAGCTCCAGA AGATTGACAA
ATCTGAGGGC
10 721 CGCTTCCATG TCCAGAACCT TAGCCAGGTG GAGCAGGATG GCGGAGCGGG
GCATGGACTC
781 CGCAGATCTT CCAAGTCTG CTTGAAGGAG CACAAGCCC TCAAGACGTT
AGGCATCATC
15 841 ATGGGCACTT TCACCTCTG CTGGCTGCC TTCTTCATCG TTAACATTGT
GCATGTGATC
901 CAGGATAACC TCATCCGTAA GGAAGTTTAC ATCTCTCTAA ATTGGATAGG
CTATGTCAAT
20 961 TCTGGTTTCA ATCCCTTAT CTACTGCGG AGCCAGATT TCAGGATTGC
CTTCCAGGAG
1021 CTCTGTGTC TGCAGCGTG TTCTTTGAAG GCCTATGGCA ATGGCTACTC
CAGCAACGGC
1081 AACACAGGGG AGCAGAGTGG ATATCACGTG GAACAGGAGA AAGAAAATAA
ACTGCTGTGT
25 1141 GAGACCTCC CAGGCACGGA AGACTTTGTG GGCCATCAAG GTACTGTGCC
TAGCGATAAC

last B2AR linker

sequence
30 1201 ATTGATTAC AAGGGAGGAA TTGTAGTACA AATGACTCAC TGCTAGAGCG
TGCGCCAGAG

PstI +5 toxR (5-141)

1261 GTCACCAACC TGCAGGGACA CAACTCAAAA GAGATATCGA TGAGTCATAT
35 TGGTACTAAA

1321 TTCATTCTTG CTGAAAAATT TACCTTCGAT CCCTAAGCA ATACTCTGAT
TGACAAAGAA
40 1381 GATAGTGAAG AGATCATTCG ATTAGGCAGC AACGAAAGCC GAATCTTTTG
GCTGTCTGGCC
1441 CAACGTCCAA ACGAGGTAAT TTCTCGCAAT GATTTCGATG ACTTTGTTTG
GCGAGAGCAA
1501 GGTTTTGAAG TCGATGATTC CAGCTTAACC CAAGCCATTI CGACTCTGCG
45 CAAATGCTC
1561 AAGATTTCGA CAAAGTCCCC ACAATACGTC AAAACGGTTC CGAAGCGCGG
TTACCAATTG
1621 ATCGCCCGAG TGGAAACGGT TGAAGAAGAG ATGGCTCGCG AAAACGAAGC
TGCTCATGAC

50

stop SD XhoI +1 GS1 alpha
1681 ATCTCTTAAT AATCAAGGAG GCCCTCGAGA TGGGCTGCCT CGGGAACAGT
AAGACCGAGG

55

1741 ACCAGCGCAA CGAGGAGAAG GCGCAGCGTG AGGCCAACAA AAGATCGAG
AAGCAGCTGC
1801 AGAAGGACAA GCAGGTCTAC CGGCGCACGC ACCGCTGCT GCTGCTGGGT
GCTGGAGAAT

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1861 CTGSTAAAAG CACCATTTGTG AAGCAGATGA GGATCCTGCA TGTTAATGGG
TTTAATGGAG
1921 ACAGTGAGAA GGCAACCAA GTGCAGGACA TCAAAAACAA CCTGAAGAG
GCGATTGAAA
5 1981 CCATTGTGGC OGCCATGAGC AACCTGGTGC CCCCCGTGA GCTGGCCAAC
CCGAGAACC
2041 AGTTTCAGAGT GGACTACATC CTGAGTGTGA TGAACGTGCC TGACTTTGAC
TTCCCTCCCG
2101 AATTCTATGA GCATGCCAAG GCTCTGTGGG AGGATGAAGG AGTGCCTGCC
10 TGCTACGAAC
2161 GCTCCAACGA GTACCAGCTG ATTGACTGTG OCCAGTACTT CCTGGACRAG
ATCGACGTGA
2221 TCAAGCAGCG TGAATATGTG CCGAGCGATC AGGACCTGCT TCGCTGCCGT
GTCTGACTT
15 2281 CTGGAATCTT TGAGACCAAG TTCCAGGTGG ACAAAGTCAA CTTCACATG
TTTGAGTGG
2341 GTGCCAGCG CGATGAACGC CGCAAGTGA TCCAGTGCTT CAACGATGTG
ACTGCCATCA
2401 TCTTCGTGGT GGCCAGCAGC AGCTACAACA TGGTCATCCG GGAGGACAAC
20 CAGACCAACC
2461 GCCTGCAGGA GGCTCTGAAC CTCTTCAAGA GCATCTGAA CAACAGATGG
CTGCCACCA
2521 TCTCTGTGAT CTTGTCTCTC AACAAAGCAAG ATCTGCTCGC TGAGAAAGTC
CTTGTCTGGGA
25 2581 AATCGAAGAT TGAGGACTAC TTTCCAGAAT TTGCTCGCTA CACTACTCCT
GAGGATGCTA
2641 CTCCCAGGCC CGGAGAGGAC CCACGCGTGA CCGGGGCCAA GTACTTCAAT
CGAGATGAGT
30 2701 TTCTGAGGAT CAGCACTGCC AGTGGAGATG GCGGTCACTA CTGCTACCCCT
CAITTCACCT
2761 GCGCTGTGGA CACTGAGAAC ATCCGCCGTG TGTTCACGA CTGCCGTGAC
ATCAITTCAGC

Clal +5 toxR (5-141)
35 2821 GCATGCACCT TCGTCAGTAC GAGCTGCTCA TCGATGGACA CAACTCAAAA
GAGATATCGA

2881 TGAGTCATAT TGGTACTAAA TTCATTCTTG CTGAAAAATT TACCTTCGAT
40 CCCCTAAGCA
2941 ATACTCTGAT TGACAAAGAA GATAGTGAAG AGATCATTCG ATTAGGCGAC
AACGAAAGCC
3001 GAATTCCTTG GCTGCTGGCC CAACGTCCAA ACGAGGTAA TTTCTGCAAT
GATTTCATG
45 3061 ACTTTGTTTG GCGAGAGCAA GGTTTTGAAG TCGATGATTC CAGCTTAACC
CAAGCCATTT
3121 CGACTCTGCG CAAAATGCTC AAAGATTGCA CAAAGTCCCC ACAATACGTC
AAAACGGTTC
3181 CGAAGCGCGG TTACCAATTG ATCGCCCGAG TGGAAACGGT TGAAGAAGAG
50 ATGGCTCGCG

loop Stop XbaI Stem-
3241 AAAACGAAGC TGCTCATGAC ATCTCTTAAT AATCTAGAGG ATCCCCGCGC
55 CCTCATCCGA
3301 AAGGGCG

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Vibrio cholerae Pctx::lacZ reporter fusion construct

5
1 XbaI
TCTAGAGGCT GTGGGTAGAA GTGAAACGGG GTTACCAGAT AAAACAGAA
AATGATAAAA
10
3 ToxR binding repeats
61 AAGGACTAAA TAGTATATTT TGATTTTGA TTTTGATTT CAAATAATAC
AAATTATATT
15
lacZ
121 ACATTATTTAA TTGTTTGTAT CAATTATTTT TCTGTTAAAC AAAGGGAGCA
TTATATGGTA
20
181 AAGACCATGA TTACGGATTC ACTGGCCGTC GTTTTACAAC GTCGTGACTG
GGAAAAACCTT
241 GCGGTATACC AACTTAATCG CCTTGCAGCA CATCCCCCTT TCGCCAGCTG
GCGTAATAGC
301 GAAGAGGGCC GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG
25
CGAATGGCGC
361 TTTGCCCTGGT TTCCGGCACC AGAAGCGGTG CCGAAAGCTG GGCTGGAGTG
CGATCTTCTT
421 GAGGCCGATA CTGTGTCGT CCCCTCAAAC TGGCAGATGC ACGGTTACGA
TGGCCCATC
481 TACACCAACG TGACCTATCC CATTACGGTC AATCCGCGGT TTGTTCCAC
30
GGAGAATCCG
541 ACGGGTTGTT ACTCGCTCAC ATTAAATGTT GATGAAAGCT GGCTACAGGA
AGGCCAGACG
601 CGAATTATTT TTGATGGCGT TAACTCGGCG TTTCATCTGT GGTGCAACGG
35
GCGCTGGGTC
661 GGTTCAGGCC AGGACAGTCG TTGCGGTCT GAATTGACC TGAGCGCATT
TTTACCGGCC
721 GGAGAAAAAC GCCTCGCGGT GATGTCGCTG CGCTGGAGTG ACGGCAGTTA
TCTGGAAGAT
781 CAGGATATGT GCGGATGAG CGGCATTTTC CGTGAAGTCT CGTTGCTGCA
40
TAAACGACT
841 ACACAAATCA GCGATTTCCA TGTGCGCACT CGCTTTAATG ATGATTTCAG
CCGCGCTGTA
901 CTGAGGGCTG AAGTTCAGAT GTGCGCGGAG TTGCGTGACT ACCTACGGGT
45
AACAGTTTCT
961 TTATGGCAGG GTGAAACGCA GGTGCGCAGC GGCACCGCGC CTTTCGGCGG
TGAAATATC
1021 GATGAGCGTG GTGTTATGCG CGATCGCGTC ACRACTAGTC TGAACGTCGA
AAACCCGAAA
1081 CTGTGGAGCG CCGAAATCCC GAATCTCTAT CGTGCCTGCG TTGAACGCA
50
CACGCGCAGC
1141 GGCACGCTGA TTGAAGCAGA AGCCTGCGAT GTCGGTTTCC GCGAGGTGCG
GATTGAAAAAT
1201 GGTCTGCTGC TGCTGAACGG CAAGCCGTTG CTGATTCGAG GCGTTAACCG
55
TCACGAGCAT
1261 CATCTCTGCG ATGCTCAGGT CATGGATGAG CAGACAGTGG TGCAGGATAT
CCTGCTGATG
1321 AAGCAGAAAC ACTTTAACGC CGTGCCTGCT TCGCATTTAT CGAACCATCC
GCTGTGGTAC

+1

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3181 AGCCCGTCAG TATCGGCGGA ATTCCAGCTG AGCGCCGGTC GCTACCATTA
CCAGTTGGTC

5 3241 TGGTGTCAAA ATAATAACGCCCTCAT CCGAAGGGC GTCTAGA
Stop Stem-loop XbaI

SEQ ID NO.: 266

10 pMPX-74 MalE (1-28) fusion vector

2401 GAATTCAGGCGCTTTTGTAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCATATGAAAAAT
1 M K I
15 2461 AAAAAAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S
20 2521 GGCTCTCGCCAAAATCATCGAAGCCCGCTCGCAGCGCTCGGTGACGCCGAATCTAGAGA
24 A L A K I I E A R L Q A S V D A E S R D
Factor Xa PstI SalI XbaI
25 2581 TTATRAAGATGACGATGACAAATAATAGCTAGAGG (transcriptional stop)
44 Y K D D D D K
FLAG lost XbaI

pMPX-72::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI

30 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-
NheI insertion with NsiI & NheI and cloning into pMPX-72 cut with PstI
& XbaI.

35

SEQ ID NO.: 267

40 pMPX-75 MalE (1-28) fusion vector

1621 CCATACCCGTTTTTTTGGGCTAGCAGGAGGCCCTGCRATATGAAAAATAAAACAGGTGCAC
1 M K I K T G A
45 1681 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCCGCTCGGCTCTCGCCAAAA
8 R I L A L S A L T T M M F S A S A L A K
Factor Xa PstI SalI XbaI FLAG
50 1741 TCATCGAAGCCCGCTCGCAGCGCTCGGTGACGCCGAATCTAGAGATTATAAAGATGACG
Lost XbaI
1801 ATGACAAATAATAGCTAGAGG (Transcriptional stop)

55 pMPX-71::male(1-28)::FXa::PstI, SalI, XbaI::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

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Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

5

SEQ ID NO.: 268

pMPX-88 MaIE (1-28) fusion vector

10

```

                                SD   old PstI   +1
                                AGGAGGTTCTGCATATGAAAAT
                                M K I
1
15      AAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTC
      4      K T G A R I L A L S A L T T M M F S A S

                                Factor Xa   PstI       SalI       XbaI
20      GGCTCTCGCCAAAATCATCGAAGCCCGCTGCAGGCCTCGGTGACGCCGAATCTAGAGA
      24      A L A K I I E A R L Q A S V D A E S R D

      FLAG                               lost XbaI
25      TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
      stop)
      44      Y K D D D D K

```

30 pMPX-84::malE(1-28)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

35 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

50 SEQ ID NO.: 269

pMPX-93 MaIE (1-28) fusion vector

```

                                SD   old PstI   +1
                                AGGAGGTTCTGCATATGAAAAT
                                M K I
45      1
      4      AAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTC
      K T G A R I L A L S A L T T M M F S A S

                                Factor Xa   PstI       SalI       XbaI
50      GGCTCTCGCCAAAATCATCGAAGCCCGCTGCAGGCCTCGGTGACGCCGAATCTAGAGA
      24      A L A K I I E A R L Q A S V D A E S R D

      FLAG                               lost XbaI
55      TTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
      stop)
      44      Y K D D D D K

```

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5 Made by cutting TOPO NsiI-malE (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86 cut with PstI & XbaI.

10 pMPX-77 MalE (1-370 del 354-364) fusion vector

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284 F V G V L S A G I N A A S P N K E L A K

3361 AGAGTTCCTCGAAAACATATCTGCTGACTGATGAAGGTCCTGGAAGCGGTTAATAAAGACAA

304 E F L E N Y L L T D R G L E A V N K D K

5

3421 ACCGCTGGGTGCGCTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAAGATCCACGTAT

324 P L G A V A L K S Y E E E L A K D P R I

pMPX-72::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG

10 Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-72 out with PstI & XbaI.

15

SEQ ID NO.: 271

pMPX-76 MalE (1-370 del 354-364) fusion vector

20

1621 CCATACCCGTTTTTTTGGGCTAGCAGGAGCCCTGCATATGAAATAAAAAACAGGTGCAC

1 SD old PstI +1 M K I K T G A

25

1681 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCTCGGCTCTCGCCAAA

8 R I L A L S A L T T M M F S A S A L A K

1741 TCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGGTCTCGCTG

28 I E E G K L V I W I N G D K G Y N G L A

30

1801 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA

48 E V G K K F E K D T G I K V T V E H P D

1861 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT

35 68 K L E E K F P Q V A A T G D G P D I I F

1921 GGGCACACGACCGCTTTTGGTGGCTACGCTCAATCTGGCCTGTGGCTGAAATCACCCCGG

88 W A H D R F G G Y A Q S G L L A E I T P

40

1981 ACAAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCCTACGTTACAAACGGCA

108 D K A F Q D K L Y P P T W D A V R Y N G

2041 AGCTGATTGCTTACCCGATCGCTGTGGAAGCGTTATCGCTGATTTATAACAAAGATCTGC

45 128 K L I A Y P I A V E A L S L I Y N K D L

2101 TGCCGAACCCGCCAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGAAAGCGGA

148 L P N P P K T W E E I P A L D K E L K A

2161 AAGGTAAAGAGCGCGCTGATGTTCAACCTGCAAGAACCCCTACTTCACTTGGCCGCTGATTG

50 169 K G K S A L M F N L Q B E P Y T W D L T W P L I

2221 CTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGG

188 A A D G G Y A F K Y E N G K Y D I K D V

55

2281 GCGTGGATAACGCTGGCGGAAAGCGGGTCTGACCTTCTCGGTTGACCTGATTAAAAACA

208 G V D N A G A K A G L T F L V D L I K N

2341 AACACATGAATGCAGACACCGATTACTCCATCGAGAAGCTGCCCTTTAATAAAGCGGAA

2248 K H M N A D T D Y S I A E A A F N K G E

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2401 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

5 2461 ATGGTGTAAACGGTACTGCGGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGC
268 Y G V T V L P T F K G Q P S K P F V G V

2521 TGAGCGCAGGTATTACGCCCGCAGTCCGAAACAAGAGCTGGCGAAAGAGTTCTCGAAA
288 L S A G I N A A S P N K E L A K E F L E

10 2581 ACTATCTGCTGACTGATGAAGGTC TGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCG
308 N Y L L T D E G L E A V N K D K P L G A

2641 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATGG
15 328 V A L K S Y E E E L A K D P R I A A T M

2701 ^{Factor Xa PstI}
348 AAAACGCCCACTCCGCTTTCTGGTATGCCGTGCGGTATCGAAGCCCGCTGCGAGGCGCTCGG
20 348 E N A Q S A F W Y A V R I E A R L Q A S

SalI XbaI FLAG Lost XbaI

2761
2CGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGA (trxn stop)
368 V D A E S R D Y K D D D D K

25 pMPX-71::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

30 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI and NheI and cloning into pMPX-71 cut with PstI &
XbaI.

35 SEQ ID NO.: 272

pMPX-89 MalE (1-370 del 354-364) fusion vector

SD old PstI +1
40 AGGAGGTTCTGCATATGAAAAATAAAAAAGGTGCAC
1 M K I K T G A

8 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCCTCGGCTCTCGCCAAA
R I L A L S A L T T M M F S A S A L A K

45 TCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGGTCTCGCTG
28 I E E G K L V I W I N G D K G Y N G L A

AAGTCGGTTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
50 48 E V G K K F E K D T G I K V T V E H P D

AAC TGG AAG A G A A T T C C C A C A G G T T G C G G C A A C T G G C G A T G G C C T G A C A T T A T C T T C T
68 K L E E K F P Q V A A T G D G P D I I F

55 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCTGTGTGGCTGAAATCACCCCGG
88 W A H D R F G G Y A Q S G L L A E I T P

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Factor Xa PstI

348 AAAACGCCCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTGCAGGCCCTCGG
E N A Q S A F W Y A V R I E A R L Q Q A S

SalI XbaI FLAG Lost XbaI

(trxn stop) TCGACGCCGGAATCTAGAGATTATAAAGATGACGATGACAAATAATAAGCTAGAGG

pMPX-84::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-84 cut with PstI & XbaI.

SEO ID NO.: 273

pMPX-94 MalE (1-370 del 354-364) fusion vector

SD old PstI +1
AGGAGGTTCTGCATATGAAAATAAAACAGGTGCAC

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1 M K I K T G A

8 GCATCTCTCGCATTATCGGCATTAAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA
R I L A L S A L T T M M F S A S A L A K

5 28 TCGAAGRAAGGTTAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGGTCTCGCTG
I E E G K L V I W I N G D K G Y N G L A

10 48 AAGTCGGTAAGAAATTTCGAGAAAGATACCGGAATTAAAGTACCGGTGAGCATCCGGATA
E V G K K F E K D T G I K V T V E H P D

68 AACTGGAAGAGAAATTCACAGGTTGCGGCAACTGCGCATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F

15 88 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGG
W A H D R F G G Y A Q S G L L A E I T P

108 ACAAGCGTTCCAGGACAAGCTGTATCGGTTTACCTGGGATGCGTACGTTTACAACGSCA
D K A F Q D K L Y P F T W D A V R Y N G

20 128 AGCTGATTGCTTACCGGATCGCTGTTGAAGCGTTATCGCTGATTATAACAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L

25 148 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGAAAGCGA
L P N P P K T W E E I P A L D K E L K A

168 AAGGTAAAGCGCGCTGATGTTCAACCTGCAAGAACGCTACTTCACTGGCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I

30 188 CTGCTGACGGGGTTATCGGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGCTGG
A A D G G Y A F K Y E N G K Y D I K D V

208 GCGTGGATAACGCTGGCGGAAAGCGGCTCTGACCTTCCTGGTTGACCTGATTAAAAACA
G V D N A G A K A G L T F L V D L I K N

35 228 AACACATGAATGAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAA
K H M N A D T D Y S I A E A A F N K G E

40 248 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCCAACTGACACCAAGCAAGTGAATT
T A M T I N G P W A W S N I D T S K V N

268 ATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTGTTGGCGTGC
Y G V T V L P T F K G Q P S K P F V G V

45 288 TGAGCGCAGGTATTAAACGCCCCAGTCCGAACAAAGAGCTGGCGAAGAGTTCTCTCGAAA
L S A G I N A A S P N K E L A K E F L E

308 ACTATCTGCTGACTGATGAAGCTCTGGAAGCGGTAAATAAGACAACCGCTGGGTGCCG
N Y L L T D E G L E A V N K D K P L G A

50 328 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAGATCCACGTATTGCCGCCACCATGG
V A L K S Y E E E L A K D P R I A A T M

55 348 Factor Xa PstI
AAAACGCCAGTCCGCTTCTGGTATGCGGTGCGTATCGAAGCCCGCTGCGAGGCTCGG
E N A Q S A F W Y A V R I E A R L Q A S

60 (trxn stop)

SalI XbaI FLAG Lost XbaI
TCGACGCCGAATCTAGAGATTATAAAGATGACGATGACAAATATAAGCTAGAGG

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368 V D A E S R D Y K D D D D K

5 pMPX-86::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG
Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & NheI and cloning into pMPX-86
cut with PstI & XbaI.

10

SEQ ID NO.: 274

pMPX-79 TrxA (2-109 del 103-107) fusion vector

15

	SD	PstI	SalI	XbaI	+2 trxA(del
103-107)					
1		TAGCAGGAGGCCCTGCAGGCCCTCGGTCGACGCCGAATCTAGAAGCGATAAAATTATT			
1		A S V D A E S R S D K I I			
20					
61	CACCTGACTGACGACAGT	TTTGACACGGATG	TACTCAAGCGGACGGGCGATCCTCGTC		
17	H L T D D D S F D T D V L K A D G A I L V				
25					
121	GATTTCTGGGCAGAGTGGTGC	GGTCCGTGCAAAATGATCGCCCGATTCTGGATGAAATC			
37	D F W A E W C G P C K M I A P I L D E I				
30					
181	GCTGACGAATATCAGGGCAA	ACTGACCGTTGCAAACTGAACATCGATCAAAACCCCTGGC			
57	A D E Y Q G K L T V A K L N I D Q N P G				
30					
241	ACTGCGCGAAATATGGCATCGTGGTATCCGACTCTGCTGCTGTTCAAAAACGGTGAA				
77	T A P K Y G I R G I P T L L L F K N G E				
35					
301	GTGCGGGCAACCAAAGTGGGTGCACTGTCTAARAGGTCAAGTGAAGAGAACCTGGCGGAT				
97	V A A T K V G A L S K G Q L K E N L A D				

35

	FLAG	Lost XbaI	
361	TATAAAGATGACGATGACAAATAATAAGCTAGAGG		(transcriptional stop)
117	Y K D D D D K		

40

pMPX-71::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

45

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
NheI insertion with PstI & NheI and cloning into pMPX-71 cut with PstI & XbaI.

50 SEQ ID NO.: 275

pMPX-78 TrxA (2-109 del 103-107) fusion vector

	SD	PstI
55		
1	GAATTGAGCGCTTTT	TAGACTGGTCGTAATGAAATTCAGGAGGTTCTGCAGGCCTC
1		A S

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SalI XbaI +2 trxA(del 103-107)

61 GGTCTGACGCCGAATCTAGAAAGCGATATAAATTATTCACCTGACCTGACGACAGTTTGTGACAC
6 V D A E S R S D K I I H L T D D S F D T

5 121 GGATGTACTCAAAGCGGACGGGCGATCTCGTCGATTCTTCTGGCAGAGTGGTGGCTCC
26 D V L K A D G A I L V D F W A E W C G P

181 GTGCAAAATGATCGCCCGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGAC
46 C K M I A P I L D E I A D E Y Q G K L T

10 241 CGTTGCAAAACTGAACATCGATCAAAACCCCTGGCACTGCGCGCAAAATATGGCATCCGTGG
66 V A K L N I D Q N P G T A P K Y G I R G

301 TATCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAGTGGTGCCT
15 86 I P T L L L F K N G E V A A T K V G A L

FLAG

361
GTCTAAAGGTCAAGTGAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAA
20 106 S K G Q L K E N L A D Y K D D D D D K

lost XbaI
GCTAGAGG (transcriptional stop)

25 pMPX-72::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Rhamnose inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
30 NheI insertion with PstI & NheI and cloning into pMPX-72 cut with PstI
& XbaI.

35 SEQ ID NO.: 276

pMPX-90 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del

40 103-107)
AGGAGGTTCTGCGAGCCTCGGTGCGACGCCGAATCTAGAAAGCATATAAATTATTT
1 A S V D A E S R S D K I I

CACCTGACTGACGACAGTTTGTGACAGGATGTACTCAAAGCGGACGGGCGATCTCGTC
45 17 H L T D D S F D T D V L K A D G A I L V

GATTTCTGGGCAGAGTGGTGGCGTCCGTGCAAAATGATCGCCCGGATCTGGAATGAAATC
37 D F W A E W C G P C K M I A P I L D E I

GCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAATGACACATCGATCAAAACCCCTGGC
50 57 A D E Y Q G K L T V A K L N I D Q N P G

ACTGCGCCGAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAA
77 T A P K Y G I R G I P T L L L F K N G E

55 GTGGCGCAACCAAAAGTGGGTGCACTGTCTAAAGTCAAGTGAAGAGAACCTGGCGGAT
97 V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI

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stop)
117 Y K D D D D K

5 pMPX-84::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
10 NheI insertion with PstI & NheI and cloning into pMPX-84 cut with PstI
& XbaI.

SEQ ID NO.: 277

15 pMPX-95 TrxA (2-109 del 103-107) fusion vector

SD PstI SalI XbaI +2 trxA(del
103-107)

20 AGGAGGTTCTGCAGGCCCTCGGTGACGCCGAATCTAGAAGCGATAAAATTATT
1 A S V D A E S R S D K I I

17 CACCTGACTGACGACAGTTTGTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
H L T D D S F D T D V L K A D G A I L V

25 GATTTCTGGGCAGAGTGGTGCCTGCGGTGCAAAATGATCGCCCGGATTCGGATGAAATC
37 D F W A E W C G P C K M I A P I L D E I

30 57 GCTGACGAATATCAGGGCAAACGTGCAAACTGAACATCGATCAAAACCCCTGGC
A D E Y Q G K L T V A K L N I D Q N P G

77 ACTGCGCGAAATATGGCATCCGTGCTATCCGACTCTGCTGCTGTTCAAAAACGGTGAA
T A P K Y G I R G I P T L L L F K N G E

35 97 GTGCGGCAACCAAAGTGGGTGCACTGTCTAAAGGTCAGTTGAAAGAGAACCTGGCGGAT
V A A T K V G A L S K G Q L K E N L A D

FLAG Lost XbaI
40 TATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (transcriptional
stop)
117 Y K D D D D K

pMPX-86::PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG
45 Temperature inducible, clone into PstI, SalI, XbaI
+1 Met required for protein to be fused

Made by cutting TOPO PstI, SalI, XbaI::trxA (2-109 del 103-107)::FLAG-
NheI insertion with PstI & NheI and cloning into pMPX-86 cut with PstI
& XbaI.

50

SEQ ID NO.: 278

55 pMPX-80 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1
male(1-28)
2401 GAATTCAGGCGCTTTTGTAGACTGGTGTAAATGAAATTCAGGAGGTTCTGCATATGAAAAAT

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1 M K I

2461 AAAAAAGGTGCACGCATCCTCGCATTATCCGCATTAACGACGATGATGTTTTCCGCCTC

4 K T G A R I L A L S A L T T M M F S A S

5

2521 Factor Xa PstI SalI XbaI

24 GGCTCTCGCCAAATCATCGAAGCCCGCTGCAGGCCCTCGTGCAGCCGAATCTAGAAG

24 A L A K I I E A R L Q A S V D A E S R S

10 +2 trxA (2-109 del 103-107)

2581 CGATAAAATTTATTCACTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCGGACGG

44 D K I I H L T D D S F D T D V L K A D G

15 2641 GCGCATCTCGTCGATTTCTGGGAGAGTGGTGCCTCCGTGCAAAATGATCGCCCCGAT

64 A I L V D F W A E W C G P C K M I A P I

2701 TCTGGATGAAATCGCTGACGAATATCAGGCGAAACTGACCGTTGCAAAATGAACATCGA

84 L D E I A D E Y Q G K L T V A K L N I D

20 2761 TCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCGACTCTGCTGCTGTT

104 Q N P G T A P K Y G I R G I P T L L L F

2821 CAAAAACGGTGAAGTGGCGGCAACCAAGTGGGTGCACTGCTCAAAGGTCAAGTGAAGA

124 K N G E V A A T K V G A L S K G Q L K E

25

FLAG Lost XbaI

2881 GAACCTGGCGGATTATAAAGATGACGATGACAAATAATAGCTAGAGG (trxn stop)

144 N L A D Y K D D D D K

30 pMPX-72::male(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Rhamnose inducible, clone into PstI, SalI, XbaI

35 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-78 cut with PstI & XbaI.

SEQ ID NO.: 279

40 pMPX-81 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 male (1-28)

1621 CCATACCCGTTTTTTTGGCTAGCAGGAGGCCCTGCATATGAAATAAAACAGGTGCAC

1 M K I K T G A

45 1681 GCATCCTCGCATTTATCCGCATTAACGACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAA

8 R I L A L S A L T T M M F S A S A L A K

50 del 103-107 Factor Xa PstI SalI XbaI

1741 +2 trxA(2-109)

28 TCATCGAAGCCCGCTGCAGGCCCTCGTGCAGCCGAATCTAGAAGCGATAAAATATTCT

28 I I E A R L Q A S V D A E S R S D K I I

55 1801 ACCTGACTGACGACAGTTTTTGACACGGATGTACTCAAAGCGGACGGGGGATCCTCTCG

48 H L T D D S F D T D V L K A D K A D I L V

1861 ATTTCCTGGGAGAGTGGTGCCTCCGTGCAAAATGATCGCCCCGATTCATGATGAATCG

68 D F W A E W C G P C K M I A P I L D E I

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1921 CTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGATCAAAACCCCTGGCA
88 A D E Y Q G K L T V A K L N I D Q N P G

5 1981 CTGCGCCGAAATATGCGATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACGGTGAAG
108 T A P K Y G I R G I P T L L L F K N G E

2041 TGGCGGCAACCAAGTGGGTGCACTGTCTAAAGGTCAAGTTGAAAGAGAACCTGGCGGATT
128 V A A T K V G A L S K G Q L K E N L A D

10 FLAG
2101 ATAAAGATGACGATGACAAATAATAAGCTAGAGG (transcriptional stop)
148 Y K D D D D K

15 pMPX-71::male(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-
107)::FLAG
Arabinose inducible, clone into PstI, SalI, XbaI

20 Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-
NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI
& XbaI.

SEQ ID NO.: 280

25 pMPX-91 MalE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1

30 male(1-28) AGGAGGTTCTGCGATATGAAAAAT
1 M K I

4 AAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTCCGCCTC
K T G A R I L A L S A L T T M M F S A S

35 Factor Xa PstI SalI XbaI
GGCTCTCGCCAAATCATCGAAGCCGCTGCGAGGCTCGGTGCAAGCCGAATCTAGAAG
24 A L A K I I E A R L Q A S V D A E S R S

40 +2 trxA (2-109 del 103-107)

44 CGATAAAATTATTACCTGACTGACGACAGTTTIGACACGGATGTACTCAAAACGGACGG
D K I I H L T D D S F D T D V L K A D G

45 64 GCGCATCTCTCGTCGATTCTTGGGCAGAGTGGTGGGTCCGTGCAAAATGATCGCCCCGAT
A I L V D F W A E W C G P C K M I A P I

84 TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACTGAACATCGA
L D E I A D E Y Q G K L T V A K L N I D

50 TCAAAACCCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTT
104 Q N P G T A P K Y G I R G I P T L L L L F

124 CAAAAACGGTGAAGTGGCGGCAACCAAGTGGGTGCACTGTCTAAAGGTCAAGTTGAAAGA
K N G E V A A T K V G A L S K G Q L K E

55 FLAG Lost XbaI
GAACCTGGCGGATTATAAGATGACGATGACAAATAATAAGCTAGAGGTACC (trxn
stop)

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144 N L A D Y K D D D D K

pMPX-84::male(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

5 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90 cut with PstI & XbaI.

10 SEQ ID NO.: 281

pMPX-96 MaIE (1-28) MCS TrxA (2-109 del 103-107) fusion vector

15 male(1-28) SD Lost PstI +1

1 AGGAGGTTCTGCATATGAAAT M K I

20 AAAAAAGGTGCACGCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCCTC
4 K T G A R I L A L S A L T T M M F S A S

25 GGCTCTCGCAAAATCATCGAAGCCCGCTGACGGCCTCGTGCAGCCGAATCTAGAAG
24 A L A K I I E A R L Q A S V D A E S R S

+2 trxA (2-109 del 103-107)

30 44 CGATAAAATTATTCACCTGACTGACGACAGTTTGTACACGGATGTACTCAAAGCGGACGG
D K I I H L T D D S F D T D V L K A D G

64 GCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCAGTCCGTGCAAAATGATGCCCCGAT
A I L V D F W A E W C G P C K M I A P I

35 TCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAAACCTGAACATCGA
84 L D E I A D E Y Q G K L T V A K L N I D

104 TCAAAACCCCTGGCACTGCGCGCAAAATATGGCATCCGTGGTATCCGACTCTGTGCTGTT
Q N P G T A P K Y G I R G I P T L L L F

40 CAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTGTCTAAAGTCAGTTGAAAGA
124 K N G E V A A T K V G A L S K G Q L K E

45 FLAG Lost XbaI
GAACCTGGCGATTATAAAGATGACGATGACAAATAATAAGCTAGAGGTACC (trxn
stop)
144 N L A D Y K D D D D K

pMPX-86::male(1-28)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

50 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-28)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

55

SEQ ID NO.: 282

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Factor Xa
3481 TGCGCCACCATTGGAACGCCAGTCCGCTTCTGGTATCCGTGCGTATCGAAGCCCG
344 A A T M E N A Q S A F W Y A V R I E A R

5 PstI SalI XbaI +2 trxA (2-109 del 103-107)
3541 CCTGCAAGGCTCGGTGACGCCGAATCTAGAAGCGATAAAATATTCACTGACTGACGA
364 L Q A S V D A E S R S D K I I H L T D D

10 3601 CAGTTTGTACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGA
384 S F D T D V L K A D G A I L V D F W A E

3661 GTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGTGACGAATATCA
404 W C G P C K M I A P I L D E I A D E Y Q

15 3721 GGGCAAACCTGACCGTTGCAAACTGAACATCGATCAAAACCTGGCACTGCGCCGAATA
424 G K L T V A K L N I D Q N P G T A P K Y

3781 TGGCATCCGTGGTATCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAA
444 G I R G I P T L L L F K N G E V A A T K

20 3841 FLAG
AGTGGGTGCACTGTCTAAAGGTCAAGTGAAGAGAACCTGGCGGATTATAAAGATGACGA
464 V G A L S K G Q L K E N L A D Y K D D D

25 3901 TGACAAATAATAAGCTAGAGG (transcriptional stop)
484 D K

pMPX-72::male(1-320 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109
del 103-107)::FLAG
30 Rhamnose inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-maleI (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-MheI insertion with NsiI & XbaI and cloning into pMPX-78
cut with PstI & XbaI.

35

SEQ ID NO.: 283

pMPX-82 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

40 SD Lost PstI +1 male (1-370 del
352-362)
1621 CCATACCCGTTTTTTTGGGCTAGCAGGAAGCCCTGCGATATGAAAAATAAAACAGGTGACAC
1 M K I K T G A

45 1681 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTTCCGCTCGGCTCTCGCCAAA
8 R I L A L S A L T T M M F S A S A L A K

1741 TCGAAGAAGGTAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATACGGTCTCGCTG
50 28 I E E G K L V I W I N G D K G Y N G L A

1801 AAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
48 E V G K K F E K D T G I K V T V E H P D

55 1861 AACTGGAAGAGAAATCCCAAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
68 K L E E K F P Q V A A T G D G D P D I I F

1921 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCGG
88 W A H D R F G G Y A Q S G L L A E I T P

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CTAGAGG (transcriptional stop)

10 Made by cutting TOPO NsiI-malE (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-79 cut with PstI & XbaI.

pMPX-92 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

265/268

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2401 CAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCCAGCAAAAGTGAATT
248 T A M T I N G P W A W S N I D T S K V N

2461 ATGGTGTACCGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTGTTGGCGTGC
5 268 Y G V T V L P T F K G Q P S K P F V G V

2521 TGAGCGCAGGTATTAACGCCCCAGTCCGAACAAAGAGCTGGCGAAAGAGTTCTCTCGAA
288 L S A G I N A A S P N K E L A K E F L E

2581 ACTATGCTGACTGATGAAGGCTCGAAGCGGTTAATAAAGACAAACCGTGGGTGCCG
10 308 N Y L L T . D E G L E A V N K D K P L G A

2641 TAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACCATTGG
328 V A L K S Y E E E L A K D P R I A A T M

15

2701 Factor Xa PstI
348 AAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCCGCTTCGAGGCCCTCGG
E N A Q S A F W Y A V R I E A R L Q A S

20

2761 SalI XbaI +2 trxA (2-109 del 103-107)
368 TCGACGCCGAATCTAGAAAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACACGG
V D A E S R S D K I I H L T D D S F D T

2821 ATGTACTCAAAGCGGACGCGGCGATCCTCGTTCGATTCTGGGCAGAGTGGTGGCGTCCGT
25 388 D V L K A D G A I L V D F W A E W C G P

2881 GC AAAAATGATCGCCCGATTCTCGATGAATCGCTGACGAATATCAGGGCAAACACTGACCG
408 C K M I A P I L D E I A D E Y Q G K L T

2941 TTGCAAAACTGAACATCGATCAAAACCTGGCACTGCGCCGAATATGGCATCCGTGGTA
30 428 V A K L N I D Q N P G T A P K Y G I R G

3001 TCCCGACTCTGCTGCTGTTCAAAAACCGTGAAGTGGCGGCAACCAAGTGGGTGCACTGT
35 448 I P T L L L F K N G E V A A T K V G A L

3061 FLAG
468 CTAAAGGTCAAGTGAAGAGAACCTGGCGGATTATAAAGATGACGATGACAAATAATAAG
S K G Q L K E N L A D Y K D D D D K

40

Lost XbaI
CTAGAGGTACC (transcriptional stop)

pMPX-84::male(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109
del 103-107)::FLAG

45 Temperature inducible, clone into PstI, SalI, XbaI

Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI,
XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-90
cut with PstI & XbaI.

50

SEQ ID NO.: 285

55 pMPX-97 MalE (1-370 del 354-364) MCS TrxA (2-109 del 103-107) fusion vector

SD Lost PstI +1 male (1-370 del
354-364)
AGGAGGTTCTGCATATGAAATAAAAACAGGTGCAC

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1 M K I K T G A

8 GCATCCTCGCATTATCCGCATTAAACGACGATGATGTTTCCGCCTCGGCTCTCGCCAAA
R I L A L S A L T T M M F S A S A L A K

5 28 TCGAAGAAGGTAAACTCGTAATCTGGATTAAACGCGATAAAGGCTATAACGGTCTCGCTG
I E E G K L V I W I N G D K G Y N G L A

10 48 AAGTCGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATA
E V G K K F E K D T G I K V T V E H P D

68 AACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCT
K L E E K F P Q V A A T G D G P D I I F

15 88 GGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCTGTGGCTGAAATCACCCCGG
W A H D R F G G Y A Q S G L L A E I T P

108 ACAAGAGGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAAACGGCA
D K A F Q D K L Y P F T W D A V R Y N G

20 128 AGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGTTTATAACAAGATCTGC
K L I A Y P I A V E A L S L I Y N K D L

25 148 TGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGCGCTGGATAAAGAACTGAAAGCGA
L P N P P K T W E E I P A L D K E L K A

168 AAGGTAAGAGCGCGCTGATGTTCAACCTCGAAGAACCGTACTTCACCTGGCGCGCTGATTG
K G K S A L M F N L Q E P Y F T W P L I

30 188 CTGCTGACGGGGTTATGCGTTCAAGTATGAAACGCGCAAGTACGACATTAAGACGCTGG
A A D G G Y A F K Y E N G K Y D I K D V

208 GCGTGGATAACGCTGGCGGAAAGCGGCTCTGACCTTCTGCTGACCTGATTAATAAACAA
G V D N A G A K A G L T F L V D L I K N

35 2341 AACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCTTTAATAAAGCGGAAA
228 K H M N A D T D Y S I A E A A F N K G E

2401 CAGCGATGACCATCAACGCGCCGTTGGGCATGGTCCAACATCGACACAGCAAAGTGAATT
40 248 T A M T I N G P W A W S N I D T S K V N

2461 ATGGTGTAAACGCTACTGCCGACCTTCAAGGCTCAACCATCAAAACCGTTCGTTGGCGTGC
268 Y G V T V L P T F K G Q P S K P F V G V

45 2521 TGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCGAAGAGTTCCTCGAAA
288 L S A G I N A A S P N K E L A K E F L A

2581 ACTATCTGCTGACTGATGAAGGCTCGAAGCGTTAATAAAGACAAACCGCTGGTGGCGG
308 N Y L L T D E G L E A V N K D K P L G A

50 2641 TAGCGCTGAAGTCTTACGAGGAAGATTGGCGAAGATCCACGTATTGCCCGCACCATGG
328 V A L K S Y E E E L A K D P R I A A T M

55 2701 Factor Xa PstI
348 AAAACGCCAGTCCGCTTTCTGGTATGCCGTGCGTATCGAAGCCGCCCTGCGGCTCGG
E N A Q S A F W Y A V R I E A R L Q A S

2761 SalI XbaI +2 trxA (2-109 del 103-107)
368 TCGACCGCGAATCTAGAAGCGATAAAATATTCACTGACTGACGACAGTCTTTGACACGG
V D A E S R S D K I I H L T D D S F D T

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15 3061 C T A A A G G T C A G T T G A A A G A G A A C C T G G C G G A T T A T A A A G A T G A C G A T G A C A A A T A A T A A G _
468 S K G Q L K E N L A D Y K D D D D K

CTAGAGGTACC (transcriptional stop)

20 pMPX-86::malE(1-370 del 354-364)::FXa::PstI, SalI, XbaI::TrxA(1-109 del 103-107)::FLAG

Temperature inducible, clone into PstI, SalI, XbaI

25 Made by cutting TOPO NsiI-male (1-370 del 354-364)::FXa::PstI, SalI, XbaI::FLAG-NheI insertion with NsiI & XbaI and cloning into pMPX-95 cut with PstI & XbaI.

30